Phosphoproteomic profiling of BCR signalling identifies ARPC5 proteins as mediators of B cell migration

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by

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Background: B-cell receptor signalling has a central role in the pathogenesis of B cell malignancies, a role that is therapeutically exploited with the introduction of compounds that target the signalling pathways emanating from this receptor. At the beginning of this thesis our understanding of BCR signalling was based on targeted studies of individual molecules whose findings have been compiled into pathways.

Aim: To use a discovery proteomics approach to globally characterize BCR signalling and identify new associations and events linked to BCR stimulation.

Method: A quantitative phosphophroteomic workflow using SILAC technology, protein isolation by immunoprecipitation with antiphosphotyrosine antibodies and characterization with mass spectrometry.

Results: A snapshot of signalling within a B-cell line was captured after BCR stimulation and compared to signalling within resting B cells. I here describe a proteomic dataset totalling 854 proteins, 60 of which were responsive to BCR stimulation. Data analysis linked together well-established players of BCR signalling, but also highlighted the importance of cytoskeletal proteins within this dataset. In particular, members of the Arp2/3 complex, an important regulator of cellular motility that initiates polymerization of new actin filaments, were highly represented within the group of BCR responsive proteins. My interests focused on the role of ARPC5L within this complex because this protein was the fifth most abundant protein within the proteomics dataset. ARPC5L has a paralog ARPC5A, and I next investigated the role of these proteins in cell migration assays where expression of one or the other of these paralogs was reduced by treatment of cells with siRNA. I found that reduction of ARPC5A increased cell migration of MCF7 cells within wound healing

assays and of a B-cell line in assays of chemokinesis. Further study of these paralogs in MCF7 cells and MAVER-1 cells showed that manipulation of their expression changed the phenotype of these cells; knockdown of ARPC5L in MAVER-1 cells inhibited the ability of these cells to organize cytoskeleton in response to BCR crosslinking. This change in ability had impact on the way these cells responded to chemokine. Under normal circumstances B cells arrest migration to chemokine when they encounter BCR engagement. This phenomenon was preserved when ARPC5A expression was reduced with siRNA, but was reversed when ARPC5L expression was similarly reduced. I then attempted to translate these findings to Chronic Lymphocytic Leukaemia cells. I found that such cells variably expressed different ratios of ARPC5L/ARPC5A however this did not correlate with clinical staging.

Conclusions: The results of the experiments performed in this thesis characterize the role of ARPC5 isoforms, components of the Arp2/3 complex, within the mechanism contributing to the control of cytoskeletal dynamics by BCR engagement and chemokine receptor. Variation in the ratio of ARPC5L/ARPC5A expression in primary CLL cells and the different ability of CLL clones to migrate to chemokine in the presence of BCR engagement could suggest a potential role for ARPC5L within the pathophysiology of CLL although no direct correlation was found in this study. Thus, the work in this thesis provides a foundation to further understand the role and function of ARPC5L in both health and disease.

List of abbreviations

ABC DLBCL	Activated B-cell Diffuse Large B-cell lymphoma
AbC	Antibody control
AM	Acetoxymethyl ester
BCR	B-cell receptor
BCR-XL	B cell receptor crosslinking
BrdU	Bromodeoxyuridine
BSA	Bovine serum albumin
CCLE	Cancer Cell Line Encyclopaedia
CLL	Chronic Lymphocytic Leukamia
Das	Dasatinib
DMEM	Dulbecco's Modified Eagle Medium
DMSO	Dimethylsulfoxide
EBV	*Epstein–Barr* virus
EDTA	Ethyenediaminenetetraacetic acid
EGF	Epidermal growth factor
FACS	Fluorescence-activated cell sorting
FCS	Foetal calf serum
FITC	Fluorescein isothiocyanate
FL	Follicular lymphoma
GCB DLCL	Germinal center B-cell Diffuse large B-cell lymphoma
GFP	Green fluorescent protein
GO	Gene ontology
H/L	Heavy/Light SILAC ratio

ICGC	International Cancer Genome Consortium
LC-MS	Liquid Chromatography-Tandem Mass Spectrometry
LcK-I	Lck inhibitor
M-CLL	B-CLL with mutated IgHV genes
MHC	Major histocompatibility complex
MCL	Mantle Cell lymphoma
MWCO	Molecular Weight Cutoff
NPF	Nucleating promoting factor
NT	Non-targeting control
p-Tyr	Phosphotyrosine
PAGE	Polyacrylamide gel electrophoresis
PDGF	Platelet-derived growth factor
PE	Phycoerythrin
PIP2	Phosphatidylinositol (4,5)-bisphosphate
pY	Phosphotyrosine
RabMab	Rabbit monoclonal
RT	Room temperature
Scr	Scrambled control
SFK	Src Family Kinase
SDS	Sodium dodecyl sulphate
SH2	Src Homology 2
STR	Short Tandem Repeat
sIgM	Surface IgM
SILAC	Stable isotope labeling with amino acids in cell culture
TCGA	The Cancer Genome Atlas
shRNA	Short hairpin RNA

siRNA	Small interfering RNA
Src	Scrambled control
Syk	Spleen tyrosine kinase
UM-CLL	B-CLL with unmutated IgHV gene

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1. Chapter – Introduction

After the discovery and characterization of B cells in the mid-1960s and early 1970s, a landmark finding occurred in 1976 when the discovery of a diverse repertoire of functional VDJ_H and VJ_L rearrangements encoding the B-cell receptor (BCR) was first reported (1). During these last decades of studying this complex area, signalling pathways emanating from the BCR have been proven to set in motion cascades that control normal B cell development and survival. These pathways are more recently being investigated as central pathological mechanisms in B cell malignancies (2). A variety of BCR related pathways are activated through both tonic and chronic active signalling to promote tumour survival and mechanisms of therapeutic resistance in a variety of diseases (3). Clinically, the BCR is now considered an important entity in terms of sequence, association to biomarkers and as a drive for tumour survival and resistance. This thesis examines BCR signalling, taking a phosphoproteomic approach to globally characterize this signalling to find new components.

1.1. B cell ontogeny

Haematopoiesis is a process characterized by a series of developmental stages, from pluripotent stem cells to cells differentiated and committed to a specific lineage, (Figure 1). With respect to B-cells it is expression of the genes responsible for assembly of the B cell receptor that marks the progressive cell maturation stages associated with haematopoiesis of this lineage (4).

Lymphocyte development begins from a common lymphoid progenitor, and the first stage in the B cell lineage is differentiation of the progenitor B (pro-B**)** cell (5). These cells are characterized by early expression of the first components that will later form the BCR. Initially, CD79A and CD79B, transmembrane proteins associated with mature surface expressed Ig molecules that function as scaffolds for signalling proteins are expressed on

the cell surface in association with calnexin (6). Next, the IgH gene locus, organized as DNA gene segments, commences a recombination process termed $V_H(D)J_H$ recombination (7). Within the pro-B cells this gene first undergoes D-J joining to be followed by joining of a V segment to the D-J_H recombinant DNA (late pro-B cells) (8). When such V-DJ recombination results in translation of the heavy Ig chain protein, pro-B cells progress to the precursor B (pre-B) cell stage with expression of the pre-B cell receptor (pre-BCR) (9). The pre-BCR consists of a full-length heavy chain expressed together with the surrogate light chains, λ5 and VpreB (Figure 2) (10). Signalling through this type of receptor results in a proliferation phase (pre-BI cells) and initiates immunoglobulin-light chain (Igl*)* rearrangement (pre-BII cells) (11). At this point within the differentiation pathway of B cells comes a checkpoint whereby BCR is tested for autoreactivity (12). Strong interaction with surrounding autoantigens results in induction of apoptosis and removal of these B cell clones (13). There will be B cell clones where the BCR experiences weaker autoantigen interaction, which results in induction of receptor anergy where the BCR no longer effectively signals (14). These clones together with clones where antigen is not perceived by the BCR (naïve B cells) differentiate to transitional B cells, which then leave the bone marrow and migrate to the periphery. In the periphery anergic B-cells die because appropriate survival signals are no longer present, naïve B-cells migrate to lymphoid organs where they encounter antigen and become either memory B-cells or antibody-producing plasma cells (15). If naïve B cells fail to find cognate antigen they also die from neglect (16).

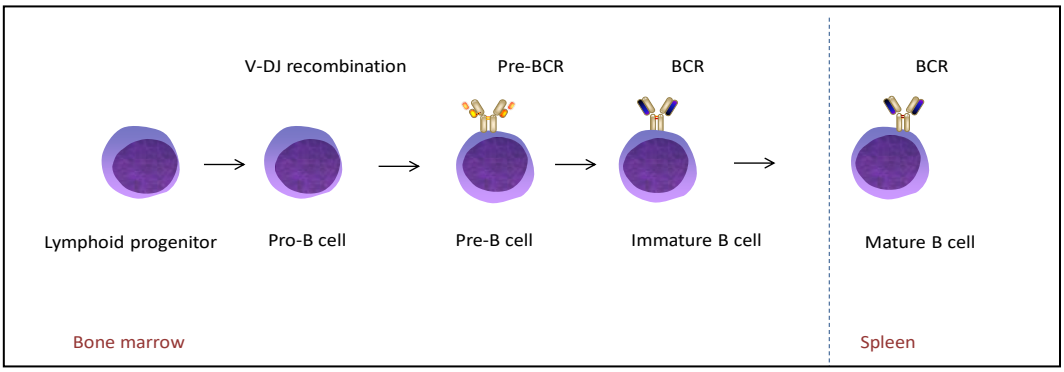


Figure 1: B cell ontogeny. Human B cells arise in primary lymphoid tissue (e.g. human foetal liver and foetal/adult marrow) and further develop in secondary lymphoid tissue (e.g. human lymph nodes and spleen). The final developmental stage is marked by antibody production by terminally differentiated plasma cells from committed pro-B cells that proliferate in response to hematopoietic growth factors and rearrange IGH V, D and J gene segments. Adapted from (17)

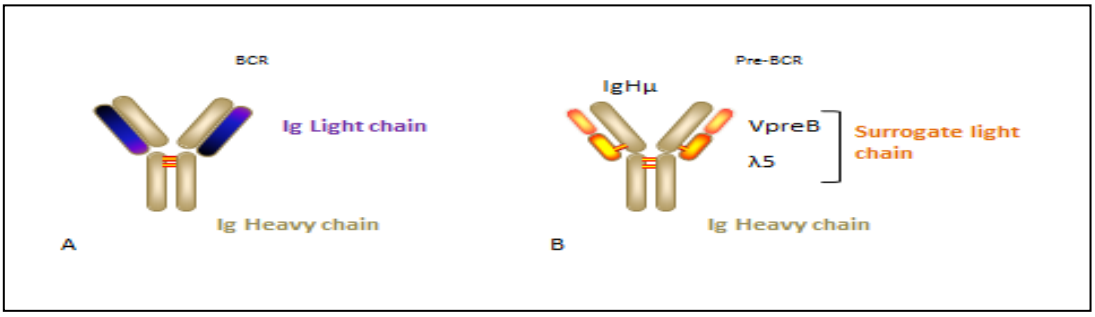


Figure 2: Pre-BCR and BCR structure. The BCR of mature B cells is a disulphide-linked tetramer composed of two identical heavy and two identical light chains. The membrane immunoglobulin is linked to the Igα/Igβ heterodimer, which contains immunoreceptor tyrosine-based activation motifs (ITAMs). B. The pre-BCR is composed of two immunoglobulin μ heavy chains (μHC), two surrogate light chains (SLC) consisting of the non-covalently associated polypeptides, VpreB and lambda5, and the transmembrane proteins Igα and Igβ. Adapted from (17).

1.2. BCR signalling

Binding of antigen to the BCR of mature B cells results in two principal signalling outputs: 1) survival and proliferation and 2) antigen internalisation (18,19). The signalling components leading to these outputs have been worked out within a constructed model examining individual contributions. The basic structure of the BCR is displayed in Figure 3 and consists of the antigen binding subunit (heavy and light chain immunoglobulins) in association with the Igα/ Igβ (79A/79B) heterodimer at the plasma membrane. The CD79A/B heterodimer contains immunoreceptor tyrosine-based activation motifs (ITAMs) within its cytoplasmic tail, motifs that initiate signal transduction when phosphorylated on tyrosine (20). These phosphotyrosine residues within the ITAMs are binding sites for SH2 (Src Homology 2) domain-containing proteins which are responsible for initiating the BCR signaling cascade (21).

Foreign particles are recognized by the B cell receptor (BCR) for antigen. Although none of the components of the BCR complex has intrinsic enzymatic activity, their engagement leads to the enhanced phosphorylation of multiple intracellular proteins on tyrosine, which occurs through the recruitment and activation of cytoplasmic protein-tyrosine kinases (22).

Specifically, for the initiation of signalling, the cytoplasmic tails of CD79A and CD79B must be tyrosine phosphorylated on the ITAMs by the Src family kinase (SFK) Lyn (23). The phosphorylation of two ITAM tyrosines results to the Syk binding to the receptor via its SH2 domains (24), a step that is necessary for signal propagation (25). What follows is formation of a signalosome whereby scaffolding proteins such as BLNK and CD19, and pleckstrin homology domain containing proteins are recruited to the BCR (26-28). Scaffolding proteins are phosphorylated by Syk and Lyn to create phosphotyrosine residues for the recruitment of downstream proteins including Bruton's tyrosine kinase (Btk), phospholipase C-γ2 (PLCγ2) and phosphatidylinositol 3-kinase delta (PI3Kδ). Activation of PI3Kδ allows conversion of phosphatidylinositol 4,5-bisphosphate (PIP_2) to phosphatidyl-inositol 3,4,5-bisphosphate (PIP_3), which then attracts PH domain containing

proteins (such as Btk and PLCγ2) to the membrane (29). Btk becomes activated through phosphorylation by Syk and catalyses activation of PLCγ2 (30). PLCγ2 hydrolyses PIP_2 to inositol 1,4,5-trisphosphate (IP3) and diacylglycerol (DAG). IP3 binds the IP3 receptor (IP3R) on the endoplasmic reticulum which causes the release of calcium from intracellular stores (31). DAG together with released calcium activates classical PKC isozymes such as PKC beta to catalyse downstream signalling to NF-κB and Jnk (32). DAG can also interact with RasGRP3, a Ras guanine nucleotide exchange factor (RasGEF), to create active Ras and eventually stimulate signalling through the Raf/MEK/ERK signalling cascade in combination with active Ras generated by Grb2-Sos. PIP_3 generated by active PI3Kδ also recruits and activates Akt to stimulate cell growth (33), as well as Vav, which generates active Rac1 to catalyse cytoskeletal rearrangement (34).

Following engagement, internalization of the BCR is observed. This allows antigen to be trafficked to endosomal compartments where it is loaded on to major histocompatibility complex proteins (MHC) to be re-expressed at the B cell surface. After being transported inside the cell, antigens encounter various proteolytic enzymes and proteolysis leads to production of antigen-derived peptide fragments. Peptides can be generated either by lysosomal proteases in the endocytic pathway, or by proteasomes when endocytosed proteins are transferred across the endosomal membrane into the cytosol. Thus, generated peptides may associate intracellularly with either MHC class I (MHCI) or MHC class II (MHCII) molecules, and in that instance, can be transferred to and displayed at the plasma membrane. In turn, the MHC-peptide complexes are able to present peptides to CD4+ T cells and antigen presentation facilitates complete activation of B cells (35).

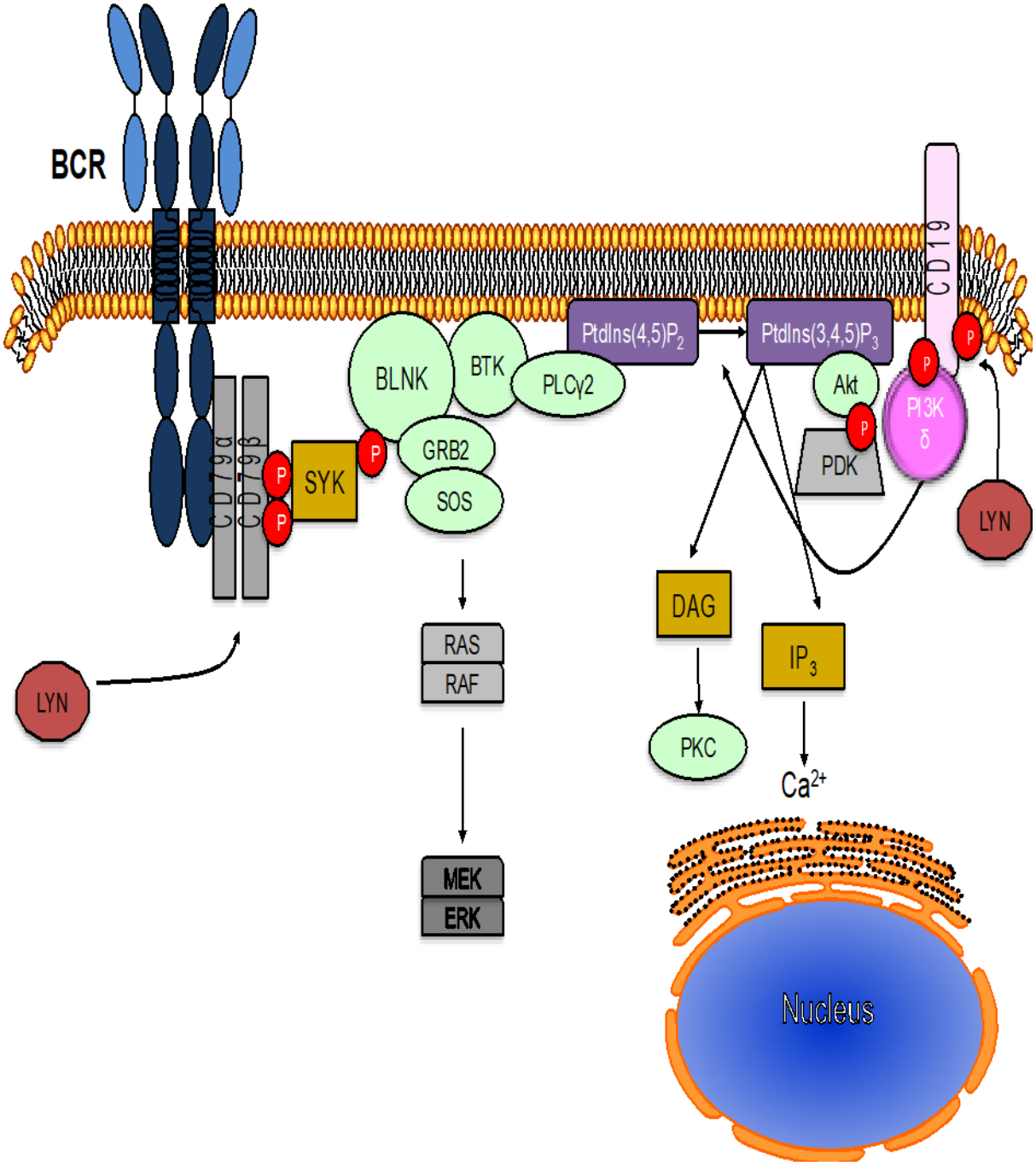


Figure 3: Overview of the B-cell receptor pathway. The BCR is composed of an immunoglobulin M molecule linked to a CD79A/CD79B heterodimer. BCR signalling is triggered upon antigen engagement, and signal initiation occurs when the tyrosine residues in the cytoplasmic ITAM portion of CD79A and CD79B are phosphorylated by kinases Lyn and Syk. This event results in the formation of a signalosome, composed by kinases and adaptor proteins, such as Syk, Btk, BLNK and Grb2. Downstream signal propagation advances

through activation of various pathways: Specifically, Syk phosphorylates the adaptor protein BLNK which allows BLNK to assemble Btk, PLCγ2 and Grb2. When these molecules are recruited, Syk is able to phosphorylate Btk to activate PLCγ2. Following its activation PLCγ2 generates IP3, which induces calcium influx from the intracellular stores in the endoplasmic reticulum as well as the extracellular environment, and DAG that activates Ras and eventually MEK/ERK. DAG also activates PKC that is responsible for activation of the IKK complex. In addition, phosphorylation of the CD19 co-receptor by Lyn causes p85, the regulatory subunit of PI3K to bind to CD19 and cause the activation of the p110δ catalytic subunit. PI3K then phosphorylates PIP2 to generate PIP3 in order to recruit more proteins via pleckstrin homology domain to propagate BCR activation (3).Refers to overleaf

1.3. Autonomous BCR signalling

In addition to antigen-dependent signalling, the BCR is also capable of autonomous responses. This type of signalling can be initiated either by self-recognition of epitopes within the BCR heavy chain, or by BCR responses to low-affinity autoantigens. In CLL, BCRs can induce antigen-independent cell-autonomous signalling, which depends on the heavy-chain complementarity-determining region (HCDR3) recognising an intrinsic motif of the BCR. (36). Autonomous signaling of BCRs within the cell membrane may promote growth and survival of the leukemic cells in CLL.

1.4. BCR signalling in malignancies

A variety of lymphomas are dependent on abnormal BCR signalling to control the survival and proliferation of their neoplastic B cells (37). Table 1 lists major subtypes of lymphoma together with the changes to the BCR or proteins within the signalling pathway that contribute to the generation of signals promoting

survival and proliferation. In some B cell malignancies, such as follicular lymphoma (FL) and activated B cell-like diffuse large B cell lymphoma (ABC DLBCL), the requirement of this signalling pathway is so great that they preferentially switch to an IgM phenotype even if they express other Ig phenotypes (38,39). Specifically, despite class-switch recombination, predominance of surface IgM expression is observed: The majority of FL cases express sIgM and a significantly lower number express sIgG, sIgA, or no sIg. This 'allelic paradox' indicates the presence of a selective pressure for sIgM expression on a B cell population that is considered a hallmark of FL (40). In ABC DLBCL mutations in the switch μ, region of the heavy chain gene affect its function to promote class switching, which usually involves deletion of part of the immunoglobulin CH region, from IgM to other isotypes. These inactivation events occur on the productive allele whereas the other IgH alleles often switch to another isotype. Thus, in ABC DLBCL, there appears to be selective pressure for expression of an IgM-BCR. This could be linked to individual signalling cascades that are induced by IgM-BCRs that lead to distinct transcriptional outcomes. IgM-BCR signalling preferentially induces pro-survival and mitogenic signals, including NF-κB, while IgG-BCR signalling favours plasma cell differentiation. NF-κB activation is the defining feature of ABC DLBCL, the aggressive molecular subtype of the disease, and thus IgM-BCR signalling may be part and parcel of this transcriptional profile (41). The NF-κB pathway in ABC DLBCL is activated through BCR signalling where the receptor activates PKCβ, which in turn phosphorylates CARD11, leading to the formation of an active CARD11-BCL10-MALT1 (CBM complex) that is central to ABC DLBCL pathogenesis as activating mutations are found in approximately 10% of ABC DLBCL tumours (42). In particular, mutations within CARD11 are known to change the structure of this protein so that the CBM complex stimulates kinase activity of IKKs and the cells become "addicted" to the NF- κB pathway (43). Cell lines representing ABC-DLBCL depend on BCR signalling and most are sensitive to ibrutinib, which was clinically effective in ~40% of ABC-DLBCL patients. (44)

In contrast to ABC DLBCL, germinal centre B-cell-like (GCB) DLBCL does not have a mutation within BCR signalling components. Nevertheless the

malignant cells of this disease have pharmacological sensitivity to inhibitors of Syk and PI3K (45,46). Whether there is direct engagement of BCR on GCB DLBCL cells is not clearly demonstrated, but signals emanating from this receptor could be the result of lectin binding to immature BCR as was recently demonstrated in follicular lymphoma (47). Like GCB DLBCL, FL cells depend on BCR signals generated by BCR engagement rather than mutations within the component signalling proteins.

With respect to mantle cell lymphoma (MCL) and CLL there is similarity in the way BCR signals are generated. The malignant cells in both diseases express BCR employing stereotypical genes, potentially indicating a role for autoantigen in driving engagement of this receptor (48). In CLL autoantigen stimulation of BCR is particularly observed in cases where the genes coding for the antigen-binding domain remain in germline configuration (so-called unmutated CLL). A similar role for autoantigen may also be present in MCL because of differences in IgHV mutation status (49).

Considering that agents targeting BCR signalling components are now entering the clinic to find use in the treatment of the above diseases and that resistance to these agents is also observed (50,51), further investigation of this signalling pathway is warranted to find new targets.

Malignancy	Evidence supporting the role of the BCR
Activated B cell-like diffuse large B cell lymphoma (ABC DLBCL)	CD79B and CD79A ITAM mutations (52); siRNA: CD79A, IgM, IgL, SYK, BTK and CARD11 (41); BCR clusters (52); high response rate to ibrutinib (53)
Chronic Lymphocytic Leukaemia	Distinct IgHV segment usage and BCR stereotypy receptors (54); high response rate to Ibrutinib (55)
Burkitt's lymphoma	siRNA: CD79A and Syk (56)
Follicular lymphoma	Idiotypic non-random IgHV sequence mutation (57); phospho-flow analysis (58)
Mantle cell lymphoma	Distinct IGHV segment usage and BCR stereotypy (48); high response rate to Ibrutinib (59)

Table 1: Evidence on the involvement of BCR signalling in B cell malignancies. Adapted from (60,61)

1.5. CLL pathobiology

Chronic lymphocytic leukaemia is the most common leukaemia in developed countries. This disease is a neoplasm of mature B cells affecting older adults at a rate of approximately 20.920 estimated new cases per 100000 people in

2016 (62) (Figure 4). In the UK, Cancer Research UK (CRUK) reports that in 2014 there were an estimated 3500 new cases of CLL diagnosed and 1000 deaths from this disease reported. Interestingly, CRUK also reports that CLL incidence rates have increased by 71% since the late 1970s (63). Because of this prevalence, and because CLL is associated with significant morbidity, this disease is considered to place clinical burden upon the National Health Service.

CLL shows a male predilection and is characterized by advanced age on onset, most commonly occurring after 65 years of age. The clinical course of patients is highly variable; some remain free of symptoms and do not require treatment for decades, whereas others have high-risk disease, quickly exhibit symptoms and need of treatment soon after diagnosis. For example, patients with a TP53 aberration, either due to deletion of chromosome 17p and/or mutation within the TP53 gene, often relapse early after receiving front-line treatment and have a median progression-free survival of less than 2 years (64). In such high-risk CLL early death can result due to therapy-related and/or disease-related complications. However, most patients have a clinical course that is in between these two extremes

Prognostic factors that can help to identify patients who require therapy relatively soon after diagnosis include certain clinical features and genetic, molecular and biochemical characteristics of the CLL cell (65). Some classical prognostic markers for CLL are CD38 and ZAP70 expression, 17p deletion/TP53 mutation (as mentioned above) and mutational status of IgHV genes (66). The current frontline treatment for CLL is FCR (fludarabine cyclophosphamide rituximab), and although the past decade has seen major advances in understanding the pathophysiology of this disease leading to the discovery of improved therapy, CLL remains incurable (67).

Analysis of IgHV gene sequences in CLL cells led to the identification of subsets of disease defined by the level of mutation from the germline sequence (68). Those cases bearing germline sequence IgHV genes are termed unmutated CLL (UM-CLL) and this is associated with more progressive disease. On the other hand, those cases bearing mutation of IgHV genes at levels greater than 2% of the germline sequence are termed mutated CLL (M-

CLL), and this is associated with more indolent disease behaviour (69). A long-term analysis showed significant differences between UM and M-CLL in terms of progression-free survival following fludarabine and rituximab chemoimmunotherapy. Thus, IGHV mutation status is a clinically relevant prognostic marker in CLL (68). Despite of its proven value to predict the course of the disease, mechanisms responsible for the differences in clinical behavior are poorly understood (70) . One of the formed hypotheses is that UM-CLL is associated with poor disease outcome because of the polyvalent antigen specificity associated with the IgHV genes used (71).

An important feature of the BCR expressed on CLL cells is that they can be highly similar between patient samples in terms of gene usage (72). In particular one third of all CLL cases display highly homologous complementarity determining region 3 genes CDR3 (73). Specifically CDR3 of the V domain of the heavy chain (VH) plays a critical role in antigen recognition: the similarity between the primary VH CDR3 sequences of two immunoglobulins translates to similarity in folding and specificities (74). Because of the vast generated diversity of the repertoire of BCR sequences due to affinity maturation the likelihood that two independent B-cell clones having identical VH CDR3 is negligible. However, in spite of this fact CLL is characterized by the existence of subsets of clones with quasi-identical (stereotyped) VH CDR3 sequences. One third of CLL patients may be categorised on the basis of sequence motifs in the VH CD3 regions. This discovery provides strong evidence for a role for a limited set of antigens on the disease ontology (75).This suggests a role for either autologous BCR signalling, or for a common antigen in the pathogenesis of this disease. This leads to greater BCR engagement on the CLL cells and contributes to disease progression, an observation supported by gene expression profiling data showing that BCR signalling is the most significantly upregulated pathway in CLL cells collected from lymph nodes, a site where disease is active (76). *In-vitro* studies of BCR activation show that this promotes CLL survival and proliferation (77), and that strong response to receptor activation correlates clinically with more aggressive disease (78). Potentially the relationship between BCR signalling and lymphadenopathy is important in CLL as in

studies looking at disease progression of patients exhibiting bulky lymphadenopathy were significantly more likely to have high disease progression than patients without this phenotype (79).

The factors controlling retention of CLL cells within lymphoid tissues are not fully clarified but BCR may play a role because of its known function in supressing normal B cell migration (80). *In vivo*, antigenic stimulation via the B-cell receptor is a major driv*er* of the proliferation and survival of CLL cells (81). Furthermore, *in-vitro c*rosslinking of the BCR with either immobilized or soluble bivalent anti-IgM $F(ab')_2$ fragments, induces B cell activation (82). Response to crosslinking is shown to be a diversifying feature between mutated and unmutated CLL cases and can predict disease prognosis (83,84).

Taken together, this evidence has made the BCR signalosome a clinically important entity and an attractive target for drug development, observations that have been exploited with the introduction of drugs such as Ibrutinib and Idelalisib targeting, respectively Btk and PI3Kδ within the BCR signalling pathway (37).

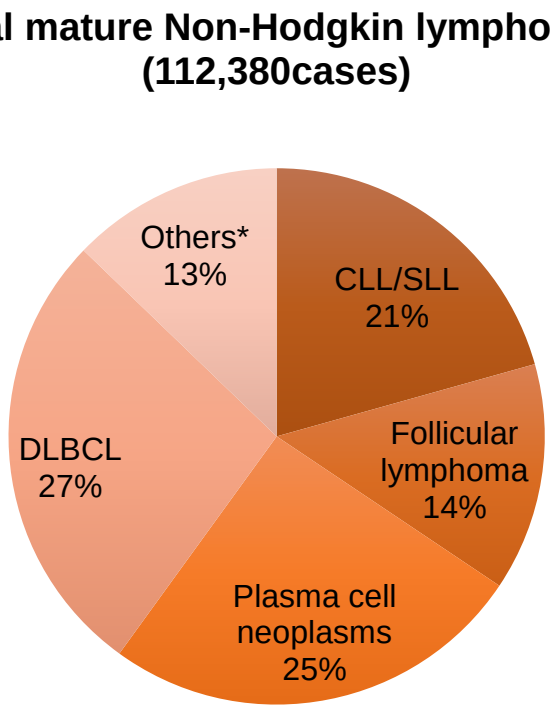


Figure 4: Estimated distribution of Mature Non-Hodgkin Lymphoid neoplasms in the US in 2016. CLL is listed as major B-cell neoplasm with 20.980 CLL/SLL cases expected to be diagnosed in 2016, in a total of 112380 mature NHL neoplasms. Adapted from (62), *Refers to Peripheral T-cell lymphoma (4%), Lymphoplasmacytic lymphoma (2%), Hairy cell leukaemia (2%), Burkitt lymphoma (1%), Others 2%.

1.6. B cell migration

Since the establishment of BCR signalling as a key player in the pathogenesis of B cell malignancies, two of the drugs targeting BCR signalling components, Ibrutinib and idelalisib have shown promise in clinical studies (85,86). Studies on their mechanism of action showed that they target BCR-controlled retention of B cells in the lymphoid organs. With ibrutinib α4β1 integrin mediated adhesion caused by chemokine or BCR induced activation is disrupted (87). This process is different than what is seen with idelalisib where the effect of BCR engagement on suppressing CLL cell egress from tissues is suppressed

(88). These observations explain the mobilization of malignant cells from their protective microenviromental niches into the circulation where they become deprived of growth and survival signals. The clinical success of these therapeutic agents reveals an important role for BCR in maintaining malignant cell residency within tissues (89). Therefore, it is important to understand how BCR affects B cell trafficking through lymphoid tissues.

Trafficking of normal B cells is regulated via the interplay between chemokine networks and BCR signalling. Specifically, migration of malignant and normal B cells to the bone marrow and secondary lymphoid tissues is controlled by CC and CXC chemokines such as CCL21 and CXCL12 (90). These chemokines bind cognate receptors, CCR7 and CXCR4 respectively, which are heterotrimeric G-protein coupled receptors which modulate intracellular pathways integral to chemotaxis (91). For example, CXCR4 signals through heterotrimeric G proteins ($G\alpha_i$ and $\beta\gamma$ subunits) facilitating the activation of PI3K-Akt, Raf/Ras/MEK1/2/ERK1/2 and some key survival pathways (92,93). These chemokines modulate the homing of B cells to tissues such as lymphnodes or spleen. Once within lymphoid tissues B cells “search” for antigen, migrating between the lymphoid follicle and the T cell rich zone. If they fail to find antigen then B cells migrate out of lymphoid tissues via a gradient of sphingosine-1 phosphate (94,95). If however antigen is found, B cells become arrested in this search and remain within tissues until contact is made with cognate CD4+ T cells, which then help the activated B cells to undergo somatic hypermutation and differentiate into either memory B cells or plasma cells (96).

In terms of modulators of B cell migration arrest, the protein HGAL (human germinal centre–associated lymphoma) has been shown to be involved in the confinement of lymphocytes to the germinal centre (97). In human cells, HGAL is highly expressed in normal B cells undergoing the germinal centre reaction, and in the malignant cells of GCB DLBCL and classical Hodgkin’s lymphoma where tumours are mainly discretely confined (98). Interestingly, HGAL is found to colocalize with actin and is a substrate of Syk (99). However, HGAL is not the only protein involved in mediating B cell migration arrest because knockdown of M17, the murine counterpart of HGAL, has only subtle effects

on B cell function and antibody production. For example, M17-/- mice have reduced-sized Peyer's patches explained by restricted egress of B cells (97,99) . Therefore, more work needs to be done to characterize the components mediating B cell migration arrest in order to fully understand how this process works.

1.7. BCR signalling and the cytoskeleton

So far in this thesis I have described the ability of BCR to act as a signal transducer and a mediator of migration arrest. Another important function of the BCR is its function as an antigen transporter. Upon antigen binding to the BCR the cortical actin network undergoes rapid and transient depolymerisation and detachment from the plasma membrane (100). This releases B cell receptors and enables them to interact with each other. Following actin disassembly, actin is reassembled at the BCR activation surface (101). *De novo* actin polymerization is activated at the outer edge of the B cell surface and enables B cells to spread and expand the contact area with the antigen-presenting surface. The extension of lamellipodia also enables the cell to gather more antigens to BCRs and eventually their contraction brings BCR–antigen complexes inwards to form larger microclusters (102). Actin-mediated B cell contraction enables the BCR microclusters to form a central cluster, which is, in turn, surrounded by de novo actin polymerization sites that facilitate internalisation and eventual translocation to the endosome (103).

Some of the links between BCR and cytoskeleton have been investigated in recent studies. In 2009, Btk was recognized as a connector transmitting signals from the BCR to actin for cytoskeletal reorganisation by regulating activity of WASP, a protein that facilitates actin nucleation by interacting with the Arp2/3 complex (described below) (104). Significantly, Btk is critical to actin cytoskeleton remodelling associated with high efficiency BCR-mediated antigen uptake, processing and presentation (105). However, other proteins

are also involved in this process. Another regulator that does not belong to the WASP family is HS1, a Lyn kinase substrate, that is overexpressed and highly phosphorylated in CLL cells (106). Both WASP and HS1 are known to interact with the Arp2/3 complex, pointing at a potential relationship with respect to BCR (107,108) .

1.8. Arp2/3 complex discovery and characterization

The Arp2/3 complex, a 220 kDa seven-protein complex comprising two actin-related proteins and five other subunits, is an important regulator of cellular motility by giving rise to polymerization of new actin filaments (109).

The complex was first discovered by Laura Machesky in protozoon *Acanthamoeba* in 1994, a finding that was independently verified by other groups in other cell systems over subsequent years. The original study assigned names to the complex subunits: actin related proteins Arp2 and Arp3, and five others referred to as p41-Arc, p34-Arc, p21-Arc, p20-Arc, and p16-Arc (ARPC1–5). All components have homologues in various eukaryotes, implying that the structure and function of the complex has been conserved through evolution. Importantly both isoforms seem to be an integral part of the Arp2/3 complex (Table 2).

1.9. Arp2/3 function

The Arp2/3 complex has been characterized as “The heart of the machine that generates the branched actin filament network responsible for pushing forward the leading edge of motile eukaryotic cells” (110). The Arp2/3 complex produces branched networks and lamellipodial cell protrusions by nucleating new actin filaments from the sides of preexisting ones (111): In particular, the complex binds to the side of an existing actin filament and commences the assembly of a new one, linking the two at a 70° angle (called the Y-branching nucleator). The pointed end of the new branch is capped by Arp2/3, but is still

able to grow at its barbed end (112). According to the existing model, ARP2 and ARP3 can each bind ATP, which then causes a conformational change in the whole ARP2/3 complex of proteins (Figure 6) (113,114) . While the function of Arp2 and Arp3 is becoming clearer, that of the rest of the subunits has not been widely studied.

In a recent study of the protein interaction network of Human Protein Kinase D2 (PKD2) the entire Arp2/3 complex was identified as a novel interactor of PKD2. PKD2 was known to phosphorylate cortactin at Ser-298 and thus regulate Arp2/3 complex-induced actin polymerization (see Chapter 1.10) However, in this study cortactin was not enriched in the cytosolic fraction of HeLa cells where all members of the complex were found. Therefore, the identification of Arp2/3 complex subunits in this dataset could point toward a direct interaction between PKD2 and the complex as well as potentially introduce a new mechanism regarding a complex PKD2-dependent assembly including NPF recruitment (115).

1.10. Activation of the Arp2/3 complex

The Arp2/3 complex has weak intrinsic actin nucleating activity and therefore needs a co-factor that facilitates filament assembly (116). This observation lead to the discovery of ActA, a bacterial protein from *Listeria* which is essential for subversion of normal actin nucleating capability within infected cells in favor of the pathogen (117). Since this initial report, additional nucleation-promoting factors (NPFs) have been identified. Type I NPFs (WASP, N-WASP, WAVE1-3, WASH, WHAMM and JMY) interact with individual actin molecules and the Arp2/3 complex via a conserved carboxy-terminal VCA domain. Functional specificity of these proteins is generated by the high divergence of protein structure outside of this VCA region verprolin homology, cofilin homology, and acidic (Figure 5). This allows them to interact with various regulatory or scaffolding proteins to activate the Arp2/3 complex. WASP and its paralogue N-WASP are of importance to B cells where they act to couple BCR to the actin network. WASP and N-WASP exhibit ~50% homology, and these two

proteins connect signalling to actin dynamics via their GTPase binding (GBD), proline rich (PRD), and pleckstrin homology (PH) domains. The binding of GTP–Cdc42 and phosphatidylinositol-4,5-biphosphate ($PI(4,5)P_2$) releases the proteins from an autoinhibitory conformation. Signalling-induced phosphorylation of WASP and N-WASP, at tyrosines in the GBD domain and at serines in the VCA, domain, is required for their optimal activity in B cells. How WASP and N-WASp are connected to BCR signalling is through the RacGEF Vav which generates GTP-Cdc42, and Btk which phosphorylates Vav and WASP (118) .

Type II NPFs such as cortactin, in contrast to type I NPFs, are weaker activators of the Arp2/3 complex and bind to filamentous actin instead of actin monomers (119). Moreover, the actin nucleating capability of type II NPFs is located within the N-terminus of these proteins (120). Proteins such as cortactin connect to cell signalling via a C-terminal SH3 domain, and to actin filaments via a region of central repeats which help target the protein to Arp2/3 complexes at branch points (121). At these sites, cortactin can act synergistically with N-WASP displacing it from Arp2/3, to enable actin filament elongation and stabilize Arp2/3 at branches. Cortactin also promotes stabilization of branched actin networks by protecting the Arp2/3 complex from coronin 1B, an actin-binding protein that inhibits the Arp2/3 complex and promotes disassembly of branched actin networks. B cells also additionally express a haemato-specific homolog of cortactin known as HS1. HS1, like cortactin, is involved in cytoskeletal reorganization and interacts with the Arp2/3 complex, and has emerged as a key molecule controlling B-cell migration and homing. HS1 is a substrate of Lyn, which phosphorylates this protein on tyrosine after BCR cross-linking. In CLL cells the phosphorylation level of HS1 relates to the clinical course of disease, hyperphosphorylated HS1 is associated with biomarkers of poor clinical outcome.

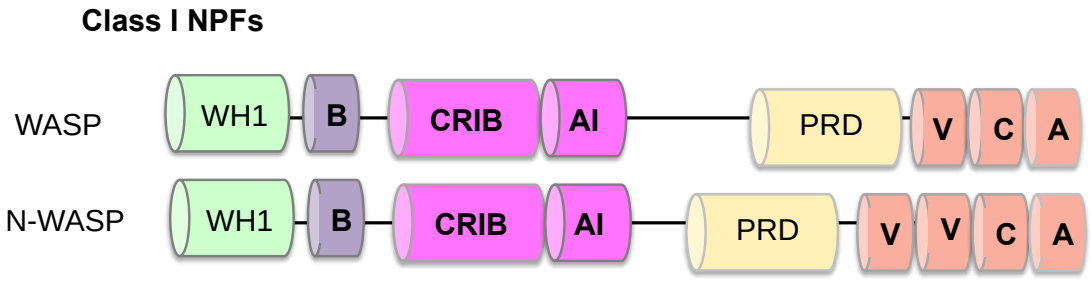


Figure 5: Class I Nucleation promoting factors of B cells. Schematic domain representation of Class I NPFs of B cells. WASP and N-WASP share a common domain organization: a N-terminal WH1 domain, a C-terminal VCA (Veprolin-cofilin-acidic) domain induces conformational changes to Arp2/3 and delivers the first actin monomer of the daughter filament (110), a Cdc42/Rac interactive binding (*CRIB)* and central B and GBD (GTP binding domain) domains. At the C-terminal, N-WASP contains a region called the VVCA domain that is composed of two verprolin homology motifs (VV); this variation causes N-WASP to show a higher intrinsic NPF activity and a much lower synergy with cortactin in comparison to WASP (122).

1.11. ARPC5 isoforms

Figure 6A shows a schematic of the Arp2/3 complex consisting of Arp2, Arp3, and 5 additional subunits. It is clear that our understanding of the roles these subunits play in the function of the Arp2/3 complex is incomplete. For the purposes of this thesis, I will concentrate on the roles of ARPC5A and its paralog ARPC5L.

Described initially in *Acanthamoeba* by the same group who discovered the Arp2/3 complex, ARPC5A and ARPC5L have been demonstrated to be encoded by different genes and share 69% sequence identity (123). In terms of tissue distribution, ARPC5A is highly expressed in spleen and thymus, whereas ARPC5L is abundant in brain where very little ARPC5A is detected. Overall ARPC5A appears to be more ubiquitously expressed in cells than is

ARPC5L, implying a functional distinction between the two isoforms. Within cells both isoforms are found in lamellipodia and cytosolic puncta as previously observed for the Arp2/3 complex (124). In addition, crystal studies of the Arp2/3 complex show that the amino acids that differ between the two isoforms are located at solvent-exposed surfaces, suggesting that ARPC5A and ARPC5L have different binding partners. These same studies showed that the intra-complex surfaces interacting with Arp2 and Arp3 seem to be conserved between the two paralogues suggesting that ARPC5A and ARPC5L affect Arp2/3 function in the same way (110). .

In terms of the function of ARPC5 isoforms, recent studies have focused on Arp2/3 complex-mediated actin filament assembly as well as disassembly of branched filament networks. By using actin-based motility of vaccinia virus as a model system and in vitro pyrene actin assembly assays, ARPC5 isoforms have been shown to differentially affect Arp2/3 complex-mediated actin filament assembly. In addition, the two paralogs also differentially affect the disassembly of branched actin filament networks by coronin 1B and1C downstream of cortactin. ARPC5 isoforms are part of functional Arp2/3 complexes that can accelerate the in-vitro assembly of actin and these complexes are characterised by different efficiencies. In the vaccinia virus model all isoform combinations can promote actin-based motility of vaccinia.and the isoform composition of the Arp2/3 complex impacts on the disassembly of the actin network. Similar correlation between different isoforms and actin assembly activity was noted for ARPC1 isoforms.

In the context of human disease, the function of ARPC5 isoforms has been explored in muscle disorders: In the course of skeletal myofiber formation or regeneration, nuclei travel from the centre to the periphery of the myofiber in order for the muscle to function. Myofiber nuclear positioning defects can lead to muscle disorders. In this context, the functional diversity linked to the different ARPC5 paralogs is observed: depletion of ARPC5L, but not ARPC5A, inhibits nuclear positioning. In addition, selective depletion of ARP5L, but not of the A paralog or control, resulted in absence of desmin organisation at the z-line. In the same study co-immunoprecipitation was used to look at interactions of the complex with γ-actin and ARPC5 isoforms. Here, ARPC5L

was shown to co-IP with actin, and the two proteins are also demonstrated to co-localise in myofibers (125).

	ARPC5A	ARPC5L
Genetic locus	1q25.2	9q34.11
Protein length	151 aminoacids	153 aminoacids
Interactors within complex	ARPC4	ARPC4
Localisation	lamellipodia	lamellipodia
Tissue distribution	Spleen, thymus,	Brain
Molecular weight recognized by antibodies	16kDa	17kDa

Table 2: Characterization of ARPC5 isoforms. Upon their discovery, ARPC5 isoforms were characterized functionally and structurally as well as in terms of tissue distribution.

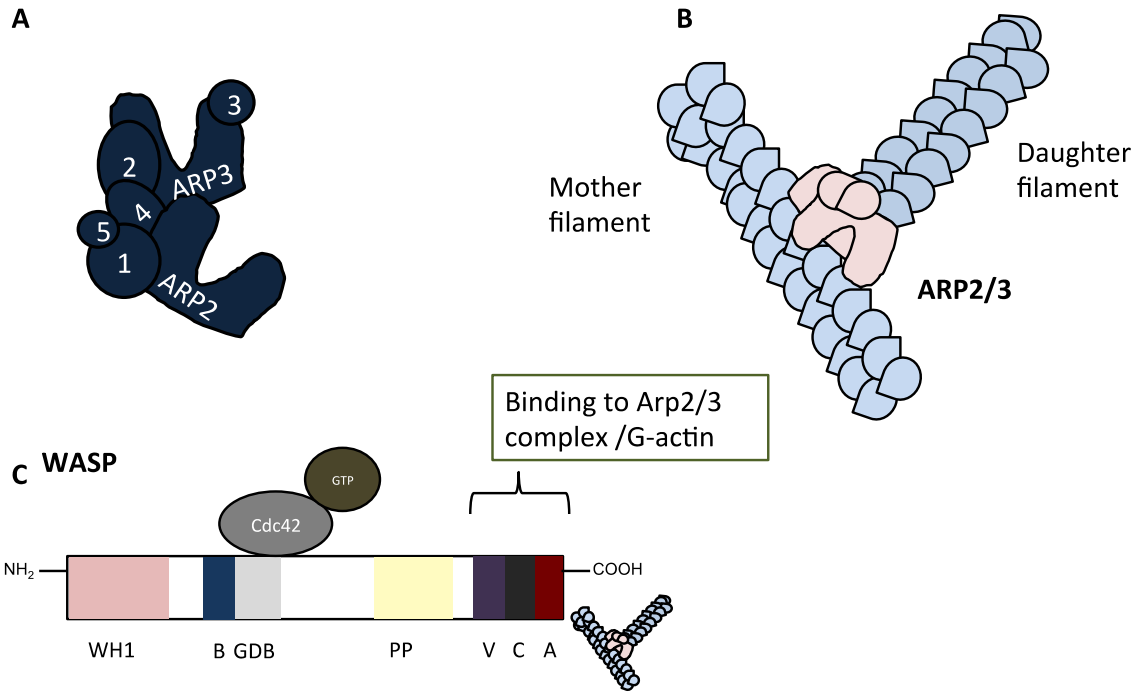


Figure 6: Organisation function and activation of the Arp2/3 complex. A. Cartoon representation of the subunit organization in the inactive Arp2/3 complex. B. Cartoon representation of new actin filament branching. Arp2/3 complex binds to the side of the mother filament and the pointed end of the daughter filament and helps point the two filaments at a 70° angle. C. Linear domain representation of WASP. WH1: WASP homology region 1, B: basic region that binds PIP2, GBD: GTPase-binding domain that binds Cdc42 and is intrinsically autoinhibited when the C region of the VCA domain binds, proline-rich domain that binds SH3 domains; V region: verprolin-homology domain that binds monomeric actin, C: central region that binds to the GBD domain in the autoinhibited state, and together with the A region, binds to and activates Arp2/3 complex to initiate an actin filament branch. Adapted from (118,126).

1.12. Phosphorylation and Arp2/3 complex

Due to the phosphoproteomic component of this study it was important to look at how posttranslational modifications regulate Arp2/3 complex activity. In order for the Arp2/3 complex to have actin-nucleating activity, the complex has to be phosphorylated, activation by NPFs as described in Chapter 1.10 is necessary but not sufficient for nucleation (127).

Experimental data has shown that different components of the Arp2/3 complex are phosphorylated in cells. For example, the p21-activated kinase (PAK) phosphorylates Thr21 in ARPC1 (128), and MAPK-activated protein kinase 2 phosphorylates Ser77 in ARPC5 (129). More recently a link has been established between phosphorylation and nucleating activity. In terms of specific residues, in the same study Arp2 phosphorylation on threonine residues (T237 and T238) was shown to be necessary for lamellipodia formation, indicating the threonine phosphorylation of the complex is necessary for nucleating activity. Importantly although phosphorylation of the Arp2/3 complex is suggested to increase cell motility, whether phosphorylation directly regulates actin nucleating activity of the Arp2/3 complex has not been reported.

In terms of how phosphorylation of the complex is regulated, EGF has been shown to induce a time-dependent but transient increase in Arp2 phosphorylation(127) Other kinases that phosphorylate Arp2 include Nck-interacting kinase (NIK), which has been shown to both phosphorylate Arp2/3 complex subunits and increase nucleation activity. NIK binds and directly phosphorylates the Arp2 subunit, which increases the nucleating activity of the Arp2/3 complex. In cells, NIK kinase activity was necessary for increased Arp2 phosphorylation and plasma membrane protrusion in response to epidermal growth factor. In contrast to Arp2, no studies have been able link the phosphorylation status of ARPC5L to nucleation.

In this thesis, ARPC5L was discovered as part of the BCR-responsive phosphoproteomics network of JeKo-1 cells. The anti-phosphotyrosine antibody enrichment strategy used quantifies phosphotyrosine proteins and

their binding partners as opposed to phosphopeptide enrichment, which specifically focuses on phosphorylated peptides (130). Therefore, to look at post-translational modifications I searched literature-curated databases for pY sites within the ARPC5L sequence in order to investigate its association with the network. PHOSIDA and PhosphoSite plus do not report a tyrosine phosphorylation site within this sequence (Figure 7), indicating that our discovery is likely the result of ARPC5L association with the network through interaction with a tyrosine-phosphorylated protein.

In this study in order to look at phosphorylation status of ARPC5L in stimulated vs unstimulated B cells, Phos-tag™ gels were used. However, I was unable to consistently observe an electrophoretic mobility shift of the phosphorylated protein.

Figure 7 Phosphorylation status of ARPC5L reported on the PHOSIDA and PhosphoSite plus databases.

1.13. Arp2/3 complex and ARPC5 isoforms in B cells

One of the first studies discussing Arp2/3 and B cells refers to the relationship between BCR clustering at the B-cell surface and actin reorganization (131).

According to the findings of this report the mechanism of this relationship is explained by the contribution of both WASP and N-WASP to activating actin polymerization during BCR engagement. According to the observations of this study, N-WASP and WASP synergize to generate and mobilize F-actin to BCR clusters during signal activation. At the B cell surface, WASP is first activated

and recruited to the B-cell contact zone by Btk, this allows WASP to win the competition for binding to Arp2/3, consequently competitively inhibiting the binding of N-WASP. However, N- WASP is involved in BCR internalization, and functions to attenuate receptor signalling following activation in the B-cell contact zone. These findings provide valuable insight into the mechanism by which the Arp2/3 complex is variously activated by WASP and N-WASP.

The role of Arp2/3 complex activation was further revealed by Obino et al, et al 2016. This study showed that Arp2/3 complex activity is required for B cells to process and present BCR-internalized antigens to T lymphocytes, suggesting a function for the complex at the B-cell synapse. When Arp2/3 is translocated at the synapse, it is partially depleted from the centrosome, thereby reducing the pool of centrosome-nucleated F-actin. According to the findings of this study the centrosome and the immune synapse compete for Arp2/3, and this competition allows the centrosome to detach from the nucleus and facilitate polarization of the cell in response to external stimuli (132). This same study showed a key component recruiting Arp2/3 to the BCR synapse is HS1, a paralogue of cortactin containing binding motifs for ARPC5 proteins and likely to interact with these proteins in the same was as described for cortactin. (132)

The role of ARPC5 paralogs in B cells is unclear but is likely to be important because genomic data derived from the Cancer Cell Line Encyclopaedia (CCLE), a collection of information from 947 human cancer cell lines (133), shows that mRNA coding for ARPC5 paralogs, and in particular ARPC5L, is most highly expressed in B cell malignancies (Figure 8) Potentially these paralogs could function in regulating actin dynamics in the same way as was recently described using a *Vaccinia* virus actin motility model. Here it is shown that ARPC5 paralogs affect Arp2/3 complex-mediated actin filament assembly as well as disassembly of branched actin filament networks. Interestingly, complexes containing ARPC5L are more efficient at nucleating actin filaments and are also better shielded against actin disassembly (134). In contrast, complexes containing ARPC5A are more susceptible to disassembly of branched actin filament networks and less able to initiate actin filament

assembly. These findings are likely to be highly relevant to the way in which cytoskeleton responds during BCR stimulation.

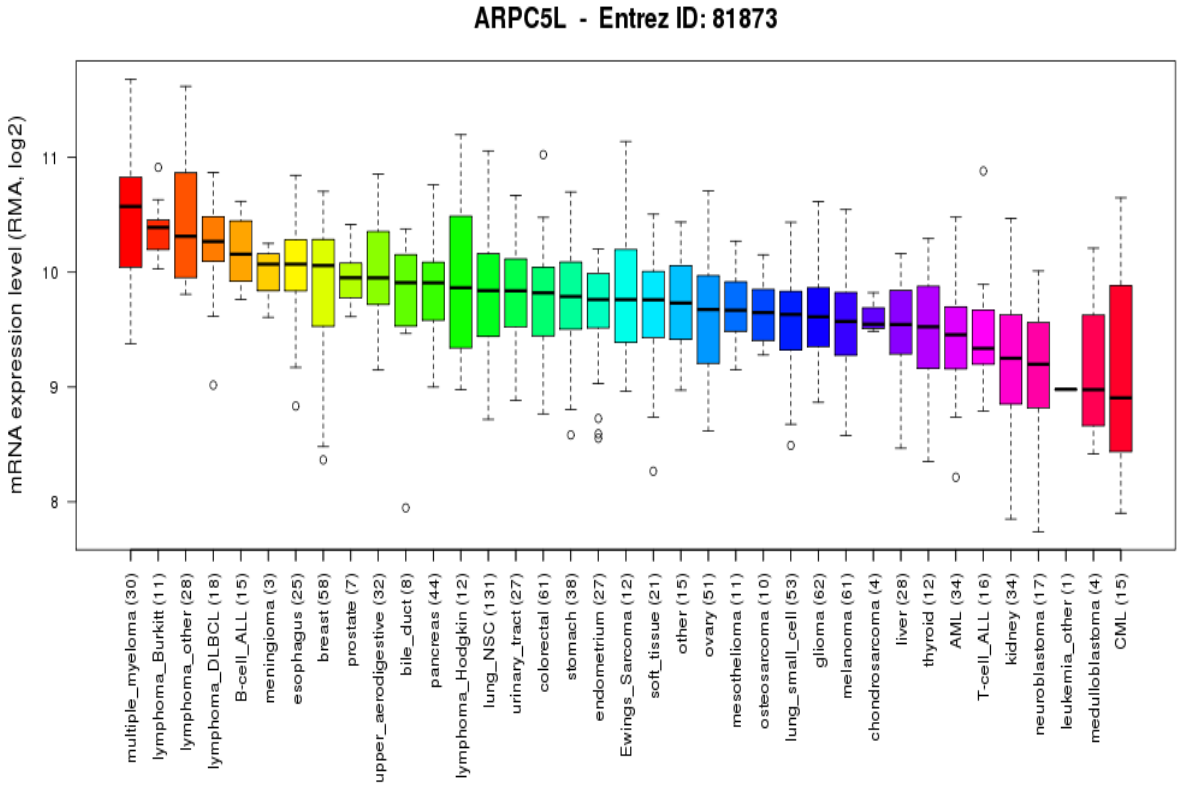


Figure 8 Characterization of ARPC5L expression in a panel of human cancer cell lines by the CCLE (Cancer Cell Line Encyclopedia). ARPC5L mRNA expression across 1000 cancer cell lines of the CCLE. Box-and-whiskers plots show the distribution of mRNA expression for each group of cell lines. The cell lines are arranged by median ARPC5L expression level (line). The boxes represent inter-quartile range and the bars up to 1.5 × the inter-quartile range. The numbers in the parentheses describe sample numbers.

1.14. ARPC5 isoforms in CLL

With respect to CLL, a study comparing responsiveness of M- and UM-CLL cells to anti-IgM stimulation identified ARPC5L as one gene among others that is significantly upregulated by such stimulation in UM-CLL cells highlighting a potential role for ARPC5L in CLL (84). More recent data suggest that ARPC5A expression may be predominant in the proliferative CLL cell fraction that emerges from lymphoid tissues during the course of disease (135), findings which warrant further investigation to establish the pathophysiological role of ARPC5 paralogs in CLL cells.

1.15. Hypothesis and aims

BCR signalling governs the fate of CLL cells as well as normal B cells and other haematological tumor cells. The central aim of my thesis was to apply a discovery proteomics approach to perform a large-scale study of BCR- related proteins to help provide global insight into disease pathogenesis and therapeutics and highlight novel targets without the bias of a preconceived hypothesis.

- The outputs of this thesis are outlined in three chapters:In the first two chapters I aimed to acquire a global snapshot of active BCR signalling in malignant B cells using a quantitative phosphoproteomics approach. Following analysis of the proteomics data, this study focused in one of the BCR crosslinking-responsive proteins ARPC5L and its isoform ARPC5A.
- In the final results chapter I hypothesized that ARPC5 isoforms affect Arp2/3 complex-mediated migration and could impact on lymphocyte trafficking towards the lymph node environment. In this chapter, I investigated the role of these proteins and their functional importance for B cell biology and aimed to transfer any functional findings in primary CLL cells, to increase the translational power of this study.

2. Chapter – Materials and Methods

2.1. Cell culture methods

2.1.1. CLL cells biobanking

Peripheral blood samples were collected from CLL patients with informed consent, and with the approval of the Liverpool Research Ethics Committee (#16/NW/0810 reviewed at Liverpool East Research Ethics Committee) and the Hull and East Yorkshire Ethics Committee (#08/H1304/35, renewed to 2023). The samples were handled according to the guidelines established by the Liverpool Leukaemia Biobank. Briefly, the whole blood sample was layered over Lymphoprep™ (Axis-Shield, Oslo, Norway) with a volume ratio of 2:1 for blood to Lymphoprep™ and then centrifuged at 800xg for 30 minutes. Lymphocytes were collected from the buffy coat layer, in the interface between the plasma and the Lymphoprep™ fraction. The white cells were diluted to 50 ml with complete medium RPMI1640 (Thermo Fisher Scientific) with the addition of 10% Foetal calf serum (FCS) (Thermo Fisher Scientific), 100 U/ml penicillin, 100µg/ml streptomycin, 0.29 mg/ml L-glutamine (Invitrogen, Paisley, Scotland), followed by centrifugation at 550xg for 5 minutes. The cell pellet was resuspended with pre-chilled RPMI-1640 medium containing 20% FCS, followed by a slow drop wise addition of an equal volume of pre-chilled RPMI-1640 medium containing 20% Dimethylsulfoxide (DMSO) (Sigma-Aldrich, UK), to a final concentration of $2x10^7$ cells/ml. The cells were distributed in 1 ml aliquots into cryogenic vials (Fisher Scientific, UK), and were initially frozen at -80°C, followed by long-term storage at -150°C (replaced by liquid nitrogen storage, after the third year of this study).

For thawing, the cryopreserved sample vials were picked from the Biobank freezer and placed within a 37°C water bath. The contents of the vials were then transferred into pre-chilled universal tubes placed in ice. Over a thirty-

minute period, pre-chilled CLL culture medium (RPMI-1640, 1% BSA, 100 U/ml penicillin, 100 µg/ml streptomycin and 0.29 mg/ml L- glutamine) was added in a drop wise manner. Subsequently, the cells were centrifuged at 550xg for 5 min at 4°C, and then washed with 5 ml of complete RPMI-1640. Finally, the cell pellets were resuspended with 5ml of complete RPMI-1640 medium, counted and the concentration was adjusted to $1x10^7$ cells/ml. Following the thawing procedure cells were left in an at normal culture conditions (5% CO_2 at 37°C) to recover for one hour. Only samples which showed more than 75% viable cells were included in further experimentation.

2.1.2. Cell lines biobanking

All cell lines (listed in table 3), were frozen down by resuspension in respective freezing medium containing 10% DMSO and stored at -150°C or liquid nitrogen. Vials of frozen cells where transferred in the waterbath at 37° to thaw briefly and then gradually resuspended in a 5 ml volume of their culture medium over a period of 2 minutes, followed by a 5 minute centrifugation at 500xg, resuspension in culture medium and another centrifugation. Finally, the cells were diluted in fresh culture medium and placed in a vented Nunc™ (T25) flask (ThermoFisher Scientific, UK).

2.1.3. CLL cells culture

Primary CLL cells were cultured in 24 well tissue culture plates (Falcon, BD Biosciences, UK), coated with non-toxic poly 2-hydroxyethyl methacrylate (polyHEMA) (Sigma Aldrich, Gillingham, UK). For the coating of the plates, 200µl of 12mg/ml poly-HEMA in 95% ethanol was added to each well (Falcon, BD Biosciences, UK) and was left to dry at 37°C overnight.

2.1.4. Cell lines culture

Nine different cell lines that were maintained in culture were included in this study (HG3, MEC-1, MAVER-1, JeKo-1, A20, Raji, Daudi, HeLa, MCF7). The JeKo-1 ATCC CRL-3006™ and MAVER-1 ACC 717™ cells were purchased from the ATCC (LGC Standards, Middlesex, UK) and DSMZ (Leibniz-Institut, Germany) respectively and were cultured according to the provider's instructions. All cell lines were kept at 37°C in an atmosphere of 5% CO_2 in a humidified cell culture incubator (standard culture conditions).

All suspension cell lines (HG3, MEC-1, MAVER-1, JeKo-1, A20, Raji, Daudi) were grown in different versions of complete RPMI-1640 medium, with the exception of MEC-1 that were cultured in Dulbecco's Modified Eagle Medium (Life Technologies, Ltd, UK) (Table 3). HeLa S3 and MCF7 cells were cultured in DMEM (Sigma Aldrich, Gillingham, UK) supplemented with 10% FBS 0.1 mM MEM non-essential aminoacids (ThermoFisher Scientific, UK). For maintenance confluent cells were split every 2-3 days at a 1:3 or 1:4 dilution. Vented Nunc™ (T25) culture flasks and 10 cm dishes were used to maintain culture.

Cell line	Origin	Culture medium
HG3	EBV-infected cells from an *IGHV1–2* unmutated CLL patient clone	complete RPMI
MEC-1	B-CLL cells in prolymphocytoid transformation to B-PLL	DMEM, 10% FCS
Daudi	16-year-old Black male patient with Burkitt's lymphoma	complete RPMI
Raji	Lymphoblast-like cells from a Burkitt's lymphoma of the left maxilla of an 11-year-old Black male.	complete RPMI
JeKo-1	Mononuclear cells of 78-year old mantle cell lymphoma patient	High glucose RPMI, 20% FCS
MAVER-1	82-year-old man with mantle cell lymphoma	complete RPMI
A20	BALB/c B cell lymphoma line derived from a spontaneous reticulum cell neoplasm found in an old BALB/cAnN mouse.	High glucose RPMI, 20% FCS
HeLa	epitheloid cervix carcinoma cells	DMEM, 10% FCS
MCF7	mammary gland, breast derived from metastatic site	DMEM, 10% FCS

Table 3: List of adherent and suspension cell lines used for the purposes of this study.

2.1.5. Cell viability and live cell concentration

Assessment of cell viability was done using Trypan blue exclusion. The cells were stained with 0.1% trypan blue (Sigma Aldrich, Gillingham, UK) at an appropriate dilution. To look at cell concentration, cell suspensions were counted using cell counting chambers (Nexcelom Bioscience Ltd, Manchester, UK)

2.2. Quality control

2.2.1. Mycoplasma detection

Routine quality control testing for Mycoplasma infection was performed every six weeks using the EZ-PCR Mycoplasma Test Kit (GeneflowLtd, Lichfieldt, UK) according to the manufacturer's instructions.

2.2.2. STR profiling

For cell line authentication purposes, the JeKo-1 cells were analysed for eight STR markers (loci): D5S818, D13S317, D7S820, D16S539, vWA, TH01, TPOX, CSF1PO and Ameloginin. To interpret STR profiling results four different databases were used: (CLIMA: Cell Line Integrated Molecular Authentication, Cogcell: Children's Oncology Group Cell Culture and Xenograft Repository, DSMZ Online Authentication of Human Cell Lines, ATCC STR Profile Database). The testing was performed by the respective service in the University of Liverpool, run by Dr Lakis Liloglou.

2.3. Western blotting

2.3.1. Preparation of whole cell lysates

Freshly thawed primary CLL cells and cells in culture were resuspended at the appropriate volume of culture medium to have $5x10^6$-$1x10^7$. During lysis, cells were kept on ice. The cells were washed once with cold PBS and lysed with 100-200ul µl of lysis buffer (1% SDS, 125 mM Tris pH 6.8, 5 mM EDTA, and 10% glycerol). The lysates were then sonicated for 30 seconds at 40% and then heated at 95 ºC for 10 minutes. Lysates were centrifuged at 14,000 rpm for 10 minutes and the supernatant was transferred to a fresh eppendorf tube for storage at -20 ºC until further use.

With regards to the lysates used for signalling studies and the immunoprecipitation experiments, serum starvation is used to synchronize cells by arresting them in the G0/G1 cell cycle phase.

2.3.2. Protein determination

The protein content of the lysates was determined using a Bio-Rad DC protein assay kit (Bio-Rad laboratories Ltd, Hertfordshire UK) following the manufacturer's instructions. Absorbance readings were taken at 650 nm, and protein concentration within the samples was determined by comparison with a standard curve prepared with BSA protein standards. Measurements were considered reliable if there was a linear doubling of absorbance with each doubling of protein standard concentration, and the correlation coefficient value for the standard curve was 0.99.

For SDS-PAGE, 10 µg of cell lysates were loaded per well. The volume of each sample applied was equalized with SDS lysis buffer, and then 5X loading sample buffer (5% SDS, 625 mM Tris pH6.8, and 50% glycerol, β-

mercaptoethanol and bromophenol blue) was added prior to boiling and gel loading.

2.3.3. Sodium Dodecyl Sulphate PolyAcrylamide Gel Electrophoresis (SDS–PAGE)

Polyacrylamide gels were prepared for a Bio-Rad minigel system (Bio-Rad laboratories Ltd, UK). Resolving gel buffer (Geneflow, Lichfield, UK) was mixed with 5.3 ml AccuGel™ 19:1 premixed Acrylamide:Bisacrylamide Solution (Geneflow) and dH_2O. 75 µl of 10% ammonium persulphate (APS) (Sigma-Aldrich, UK) and 15 µl of tetramethylethylenediamine (TEMED) (Sigma-Aldrich) were added to initiate polymerisation at room temperature. A 5% polyacrylamide stacking gel was prepared by mixing 1.5 ml stacking gel buffer (Geneflow) with 1 ml acrylamide solution and 3.5 ml H_2O, 10% APS and TEMED were then added followed by insertion of combs to form wells in the gels. The separated proteins were transferred on to ImmobilonTM Transfer Membranes (Millipore, Fisher Scientific UK Ltd, Loughborough, UK). Membranes were blocked with blocking buffer (2.5% ECL advance blocking reagent in TBS-T (150mM NaCl, 25 mM Tris pH 7.5, 0.1% Tween 20) for one hour. Commonly, the membranes were probed with primary antibodies overnight at 4º C in rotation. The following day, membranes were washed with TBS-T and then incubated with horseradish peroxidase (HRP)-conjugated secondary antibodies. The membranes were developed with Amersham ECL Western Blotting Detection Reagent (GE Healthcare Life Sciences, Buckinghamshire, UK). Chemilluminescence was read using a Fujifilm LAS-1000.

For the Arp2/3 complex work, precast polyacrylamide gels Invitrogen™ NuPAGE™ Bis-Tris 4%-12% gels were used (ThermoFisher Scientific, UK). The gels were transferred to Amersham Protran™ nitrocellulose membrane with a 0.2 µm pore size (GE Healthcare Life Sciences, Buckinghamshire, UK) and probed with primary antibodies overnight. Visualisation and quantification

was performed with an Odyssey infrared scanner (LI-COR Biosciences, Lincoln, NE).

2.3.4. Inhibitors and BCR stimulus

A $F(ab')_2$ fragment of goat anti-Human IgM (Jackson ImmunoResearch Europe Ltd, Suffolk, UK) was used throughout the thesis to stimulate the BCR. The Lck inhibitor (4-amino-5-(4-phenoxyphenyl)-7H-pyrrolo[3,2-d] pyrimidin-7-yl-cyclopentane (Lck-i)) was purchased from Calbiochem (Nottingham, UK) and used at 1 µmol/l for 2 hours. Dasatinib (BMS-354825, Sprycel) was purchased from LC laboratories (Woburn, MA, USA) and used at 150 nmol/l for two hours. All inhibitors were dissolved in DMSO, aliquoted and stored at -20°C.

2.3.5. Antibodies for detection of members of the Arp2/3 complex

Throughout this thesis RabMab® antibodies against ARPC5A (Anti-p-16 Arc [EP1551Y] ab51243, ARPC5L [EPR10274] ab169763 and ARPC2 [EPR8533] ab133315 were used for Western blotting, immunoprecipitation and immunofluorescence experiments. All antibodies were purchased from Abcam, Cambridge, UK.

3. Chapter – Identification of a cell line model to study BCR signalling in Chronic Lymphocytic Leukaemia

3.1. Introduction

Cell lines have been used extensively to look at BCR signalling, in terms of receptor kinetics (136), analysis of the function of BCR-related genes (2), drug efficacy (60), differences between tonic and active BCR signalling (4) and the pre-BCR signalling pathway (137) as well as clinical features of diseases governed by BCR signalling at the molecular level (6). Despite generation of an accepted signalling pathway (138), how this pathway functions in different types of B cells, or indeed in the malignant cells of CLL had not, at the beginning of this thesis, been fully addressed using technologies that investigate global signalling.

Obtaining global information of active BCR signalling can be accomplished by employing SILAC technology. However, one of the major limitations of SILAC is that it relies on metabolic labelling and can be used only in cell culture where the cells are metabolically active (139). CLL B cells do not spontaneously proliferate *in vitro* (140), thus SILAC cannot be used to assess BCR signalling in this cell type. Therefore, for the needs of this study I tried to identify a B cell line that mimics CLL cells in terms of BCR-associated behaviour and phenotype.

There is a small number of described B cell lines that are reported derived from B-CLL cells, and the majority of them have been immortalized with Epstein Barr virus (141,142). This fact led me; to investigate B cell lines of different origins, either from malignancies that share clinical similarity to CLL, or those whose BCR signalling resembles that in CLL cells. Daudi and Raji cells are cell lines derived from Burkitt's lymphoma, and have similarities to CLL as they are classified as a non-Hodgkin's lymphoma, and both share a

CD19+, CD20+ phenotype. Raji cells are often used in studies that examine the efficacy of BCR pathway inhibitors that are commonly used in the treatment of CLL (143). Daudi cells are known to express surface IgM and have been used in studies of BCR-mediated signalling (144). MEC-1 cells were first established and characterized in 1999 as a cell line that grew spontaneously from the peripheral blood of a patient with CLL undergoing prolymphocytoid transformation (145). These cells are a good candidate because their BCR structure is very similar to that on CLL cells. HG3 cells are derived from CD40 ligand stimulated CLL cells that have been immortalized with EBV (141). This cell line is similar to primary CLL cells in terms of phenotype. MAVER-1 and JeKo-1 cell lines are derived from MCL cells, and similarly to CLL cells they express CD5 (146,147). Finally, A20 cells are a mouse B-cell line that has been used extensively for BCR signalling studies including systems-wide analysis of BCR signalling networks (148).

In this chapter, I sought to establish a B-cell line model that approximates CLL behaviour and phenotype that is also suitable for the described SILAC labelling strategy. The first criteria for the model cell line were directly linked to BCR signalling: In particular, for this study I decided to look at the phosphorylation status of kinases such as ERK and Akt which are traditionally used as markers of BCR activation (149), Importantly, the malignant cells from approximately half of all CLL cases constitutively express pERK, such cases are characterized by cellular unresponsiveness to surface IgM (sIgM) ligation and are considered anergic (144). Typically, unmutated CLL cells that respond strongly to BCR stimulation have low basal levels of pERK (83). Therefore, the cell line for my studies should also have low basal levels of pERK prior to BCR crosslinking. Another criterion linked to events downstream of the BCR was the response to BCR pathway inhibitors. Recent work from this lab showed that the SFK Lck is a key mediator of BCR signalling in CLL cells (150). This study showed that the specific inhibitor 4-amino-5-(4-phenoxyphenyl)-7H-pyrrolo[3,2d]pyrimidin-7-yl-cyclopentane (Lck-i) blocked both proximal and distal signalling events in CLL cells following BCR stimulation. Importantly, Lck-i inhibited Lck kinase activity but had no effect on that of Lyn. Conversely, dasatinib, a pan SFK inhibitor also inhibits proximal and distal signalling in

BCR stimulated CLL cells, but inhibits both Lck and Lyn (151). Having screened the cell lines using the above criteria I then used FACS analysis to look at the immunophenotype of my selected cell line and compare it to CLL, and also confirm that the cells maintain expression of CD20 and CD19, common B cell markers used widely in the identification of B cells. In addition, anti-IgM induced calcium mobilization was used as an indicator of receptor signalling activity in the Jeko-1 cell line (152)

These experiments were performed under different physical parameters to establish an optimal crosslinking time and temperature point for my approach.

3.2. Materials and methods

3.2.1. Surface marker staining

Freshly thawed CLL cells and Jeko-1 cells were harvested, washed and their concentration was adjusted to 1-5x10^6 cells/ml in FACS Buffer (PBS, 0.5-1% BSA or 5-10% FBS, 0.1% NaN3 sodium azide), after having assessed their viability. A cell suspension of 100 µl was centrifuged at 1500 rpm for 5 min at 4°C and 5 µg/ml of the primary antibody (Table 4) or isotype control (R&D Systems Europe, Oxford, UK) was added for a 30 min incubation at room temperature in the dark. The cells were washed three times by centrifugation and resuspended in 200 µl of cold FACS buffer. Cell suspension was kept in the dark on ice until the time of analysis on a BD FACSCalibur using CellQuestPro software (BD, Oxford, United Kingdom). Table 4 lists the different FACS antibodies.

Antibody	Conjugated fluorochrome	Supplier
Mouse Anti-Human IgM	PE	BD Biosciences, United Kingdom
Mouse Anti-Human CD19	FITC	BD Biosciences, United Kingdom
Mouse Anti-Human CD5	FITC	BD Pharmingen™, United Kingdom
Mouse Anti-Human CD20	FITC	BD Pharmingen™, United Kingdom

Table 4: Details of antibodies used in FACS experiments for characterization of JeKo-1 cells surface markers expression.

3.2.2. Analysis of anti-IgM induced intracellular calcium flux

Calcium mobilization was measured using the fluorogenic probe, Fluo4-AM (Life Technologies Ltd, Paisley, UK) as a calcium indicator. JeKo-1 cells were used at 10^7 cells/ml and CLL cells were freshly thawed as described previously in complete RPMI 1640 medium at the same concentration. All cells used for this assay were incubated with 2 μM Fluo4 -AM for 30 minutes at 37°C and then washed and resuspended at 5×10^6 cells/ml at room temperature. Cells (250 μl) were placed in a waterbath at 37°C for 5 minutes prior to the first one minute acquisition which determined the basal fluorescence of non-stimulated cells, followed by addition of 20 μg/ml goat $F(ab')_2$ anti–human IgM and data acquisition for a further 5 minutes. Data were acquired on a BD FACSCalibur and analyzed using CellQuestPro. For the analysis, the percentage of cells that exhibited a spike in fluorescence following addition of anti-IgM was estimated, after having determined a background fluorescence threshold at 15% of unstimulated cells.

3.2.3. Ptyr immunoprecipitation (small scale)

For this immunoprecipitation experiment $2x10^6$ JeKo-1 cells per condition were serum starved overnight in order to achieve synchronization by arrest in the G0/G1 cell cycle phase and then crosslinked for 15 minutes. After BCR stimulation cells were kept on ice and resuspended in lysis buffer with freshly added inhibitors (Table 5) for 15 min. Following lysis, cells were centrifuged for 15min at 4°C (14000rpm) and the supernatant was collected. After carrying out a protein quantification assay, a “preclearing” step was performed to improve the immunoprecipitaton efficiency, by reducing non-specific binding to the Protein A/G agarose. Preclearing was performed by incubating the lysates with protein A for 1 hour at 4°C. A fraction of the lysate at this point was mixed with SDS-PAGE sample buffer and incubated at 95°C for five minutes (the pre-IP or input sample).

Precleared lysates were then incubated with 1µg/mg of 4G10 and 20µl of slurry protein A/G beads at 4°C in rotation. After 4 hours, p-Tyr-100 was added to the lysates and allowed to incubate for a further 2 hours. After a total of 6 hours of immunoprecipitation, the sepharose beads were pelleted. An aliquot of the supernatant was used as a post-IP sample (unbound fraction). Immunoprecipitated proteins were removed from the protein A/G beads by sequential washing with a wash buffer (Table 5). Antibody/lysate controls were prepared using the same procedure, but with non-specific antibody or with empty beads respectively. All immunoprecipitated samples were mixed with SDS-PAGE, sample buffer and boiled for 10 min.

Lysis buffer		
Components	**Concentration**	**Supplier**
Tris-Cl (pH 7.4)	20mM	Sigma-Aldrich Company Ltd, Dorset, UK
NaCl	150mM	Sigma-Aldrich Company Ltd, Dorset, UK
β-Glycerophosphate	40mM	Sigma-Aldrich Company Ltd, Dorset, UK
NaF	10mM	Sigma-Aldrich Company Ltd, Dorset, UK
IGEPAL®	1%	Fisher Scientific UK Ltd, Loughborough
Sodium deoxycholate	0.1%	Sigma-Aldrich Company Ltd, Dorset, UK
Protease inhibitor Cocktail Set V	1:50	Millipore (U.K.) Limited, Hertfordshire
Phosphatase inhibitor Cocktail Set II	1:50	Millipore (U.K.) Limited, Hertfordshire

Wash buffer		
Components	**Concentration**	**Supplier**
Tris-Cl (pH 7.4)	20mM	Sigma-Aldrich Company Ltd, Dorset, UK
NaCl	150mM	Sigma-Aldrich Company Ltd, Dorset, UK
IGEPAL®	0.1%	Fisher Scientific UK Ltd, Loughborough

Table 5: Components of buffer solutions used in immunoprecipitation experiments in chapter 3 with respective concentrations and UK suppliers.

3.2.4. Detection of surface IgM in stimulated JeKo-1 cells by flow cytometry

JeKo-1 cells were incubated with goat F(ab)'$_2$ anti-IgM at 4°C for 30 minutes and then washed to remove unbound ligand. Following the washes, the cells were incubated at 20°C for various time points (2,15,30 and 60 min). The cells were then stained with an IgM-PE antibody (BD Biosciences, Oxford, UK) as described previously and then fixed in 1% paraformaldehyde to measure expression of the remaining surface IgM in a flow cytometer. The internalization results (sIgM MFI: medium fluorescent intensity of surface IgM) were analysed using the CellQuestPro software.

3.3. Results

3.3.1. Cell lines

In the beginning of this study, I examined a variety of B cell lines in terms of BCR-regulated phosphorylation events. Antigenic stimulation of the BCR is a central part of CLL cell biology, therefore, BCR signalling response should be considered an important parameter in the quest for a CLL model cell line.

Pharmacological inhibition was used as another means of demonstrating that signalling in the model cell line is a close approximation to that in CLL cells, comparing cell lines with respect to sensitivity to Lck-i and dasatinib (see chapter 2.3.4) is also critical to identify a model of CLL signalling.

Having established the initial defining parameters for the selection of a CLL-like B cell line model (phosphorylation of Akt, ERK, response to pharmacological inhibition) I examined six B-cell lines (Table 3).

Figure 9 presents each cell line in terms of its response to BCR crosslinking and induction of pAkt and pERK. A direct comparison cannot be drawn between the protein levels in the different gels, as there is no common

reference sample between gels to allow normalisation. However, it was observed that HG3, MEC1, Raji and Daudi cells all had levels of pERK that were not further enhanced by BCR crosslinking. Daudi cells also had constitutive high levels of pAkt. In contrast in MEC1 and Raji cells levels of pAkt increased when cells where crosslinked with anti-IgM. HG3 cells remained unresponsive. Co-culture of these cell lines with Lck-i or dasatinib seemed to have little effect on constitutive phosphorylation of ERK. Taken together, these results suggest that HG3, MEC1, Raji and Daudi cells are unsuitable for further study.

I next compared JeKo-1 and A20 cells with primary CLL cells (Figure 10). Like the primary CLL cells from the case I used, Jeko-1 and A20 cells respond to BCR crosslinking with robust induction of pERK and pAkt, induction that is variously inhibited by the presence of Lck-i. Primary CLL cells showed complete inhibition of pERK and pAkt in crosslinked cells cultured in the presence of this inhibitor. JeKo-1 cells showed partial inhibition of these kinases whereas in A20 cells only induction of pERK was affected. The presence of dasatinib blocked BCR induced signalling in all the cell lines. CLL cells were also analysed for pSyk and pSrc expression to obtain additional information for the selectd case.

Taken together JeKo-1 cells appear to match the criteria set out for a model cell line of BCR signalling in primary CLL cells.

JeKo-1 cells were then taken forward for further characterization.

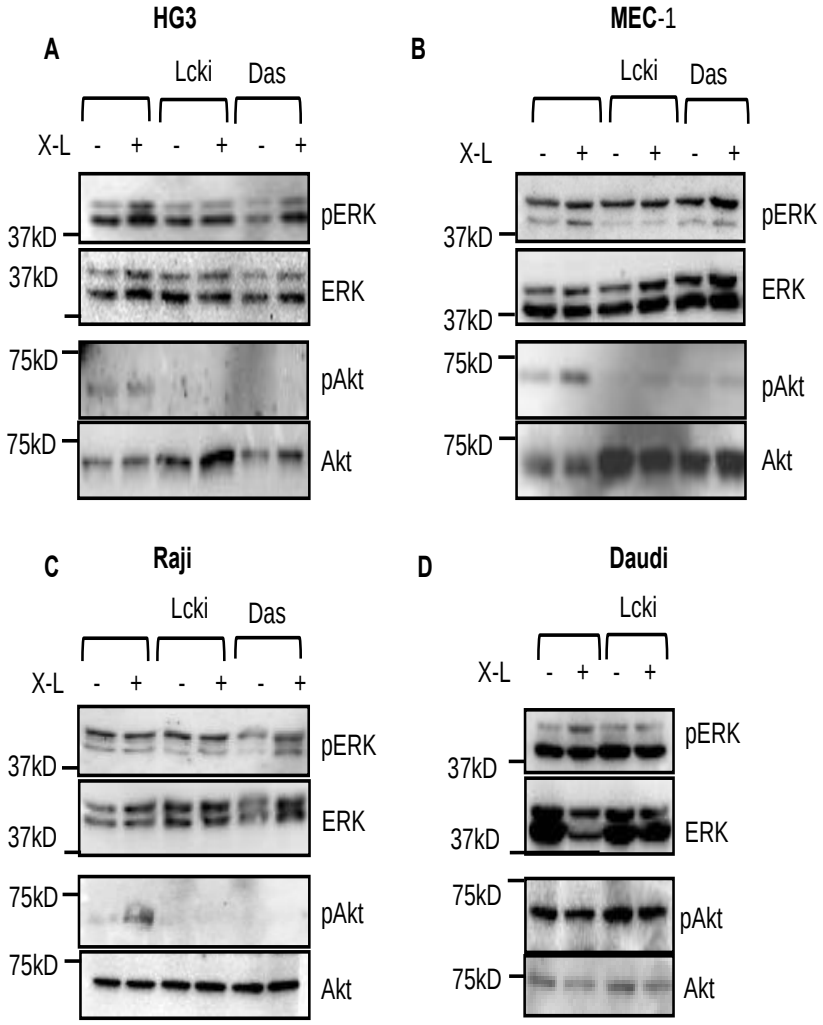


Figure 9: Phosphorylation of target proteins downstream of the BCR in different B cell lines after BCR stimulation. HG3 (A), MEC-1 (B), Raji (C), Daudi (D) cells were serum starved overnight, and on the following day incubated for 2 h in the presence of 1µM Lck-i, 150nM Dasatinib and then stimulated with 20µg/ml F(ab')2 goat anti-human IgM for 15 minutes at 37°C. The cellular lysates were analysed by Western blotting for the levels of pERK(Tyr204), pAkt(Ser473) (New England Biolabs, Hitchin, UK). Total ERK and Akt were used as loading controls.

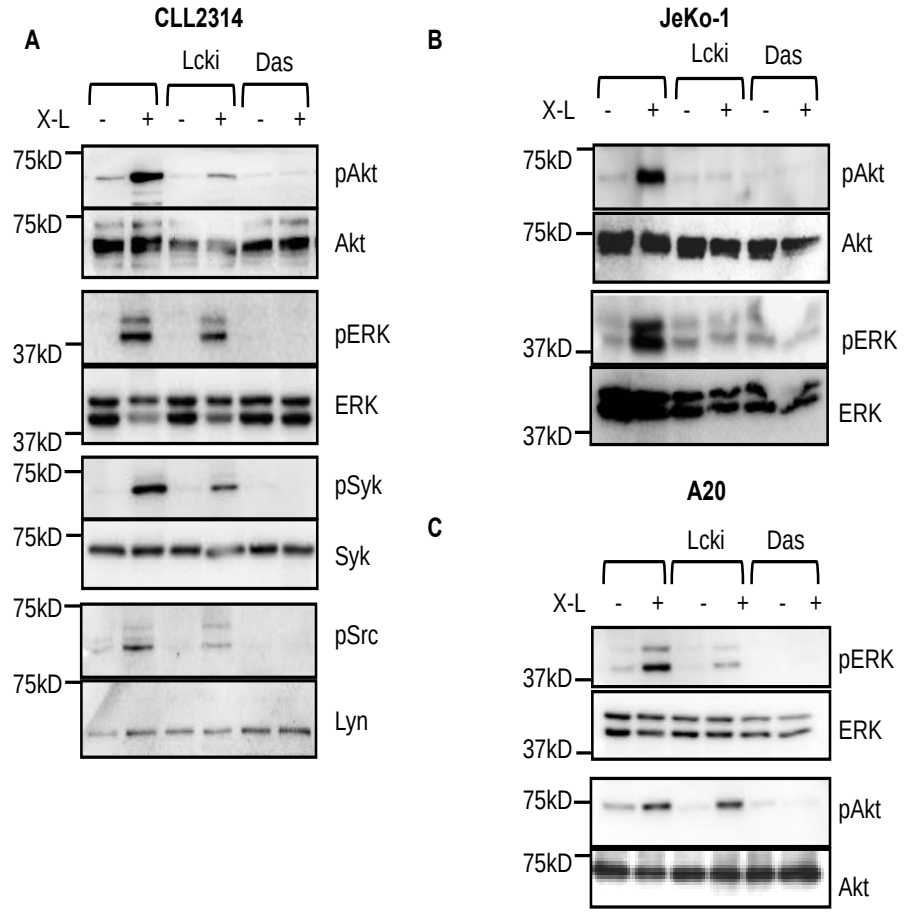
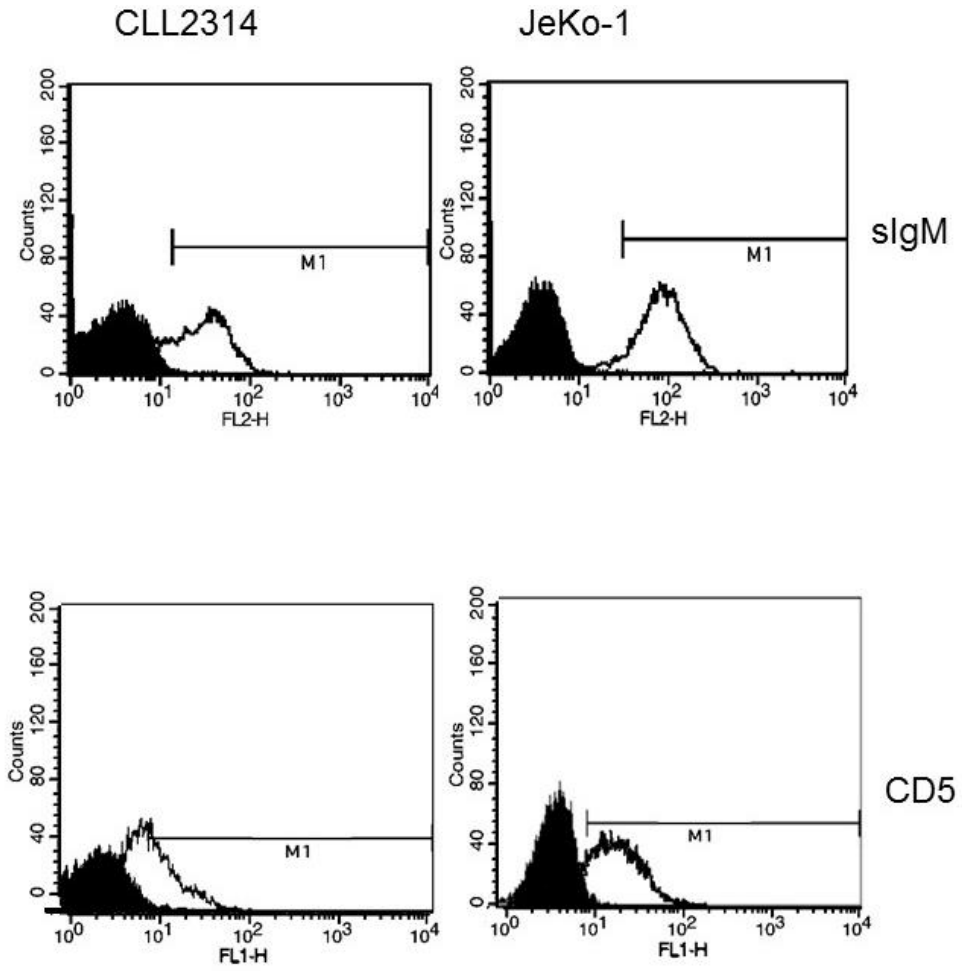


Figure 10: Stimulation of BCR in JeKo-1 and A20 cells induces similar phosphorylation of downstream BCR targets to UM CLL clones. (A) CLL cells were cultured in polyHEMA plates for 2 hours at 37° C, and then stimulated with 20µg/ml F(ab')2 goat anti-human IgM for 15 minutes at 37°C. (B), (C) JeKo-1 and A20 cells were serum starved overnight in 24 well plates and then treated accordingly. For studies with the indicated inhibitors cells were incubated for 2 h in the presence of 1µM Lck-i or 150nM Dasatinib prior to stimulation, harvest and lysis. Cell lysates were analysed as indicated for the levels of pERK(Tyr204), pAkt(Ser473), pSyk(Tyr323) and pSrc(Tyr416). All antibodies were purchased from Cell Signalling Technology (New England Biolabs, Hitchin, UK). Total Lyn, ERK and Akt were used as loading controls.

3.3.2. Surface markers

The aim of this section was to analyse the cell marker phenotype of JeKo-1 cells and compare expression of sIgM and CD5 with that expressed on CLL cells. Figure 11 shows that JeKo-1 cells are positive for CD19 and CD20 when measured by flow cytometry. These markers are specific for B cells (153) and show that JeKo-1 cells maintain a B-cell phenotype. I next compared sIgM expression and CD5 expression on JeKo-1 cells with that on primary CLL cells, I found that expression of both these epitopes is slightly reduced on CLL cells compared to JeKo-1 cells. These data show that Jeko-1 cells share important immunophenotypical characteristics with CLL.

These findings agree with the established immunophenotype described for JeKo-1 (147), and support the data indicating that JeKo-1 cells are a suitable model for CLL.



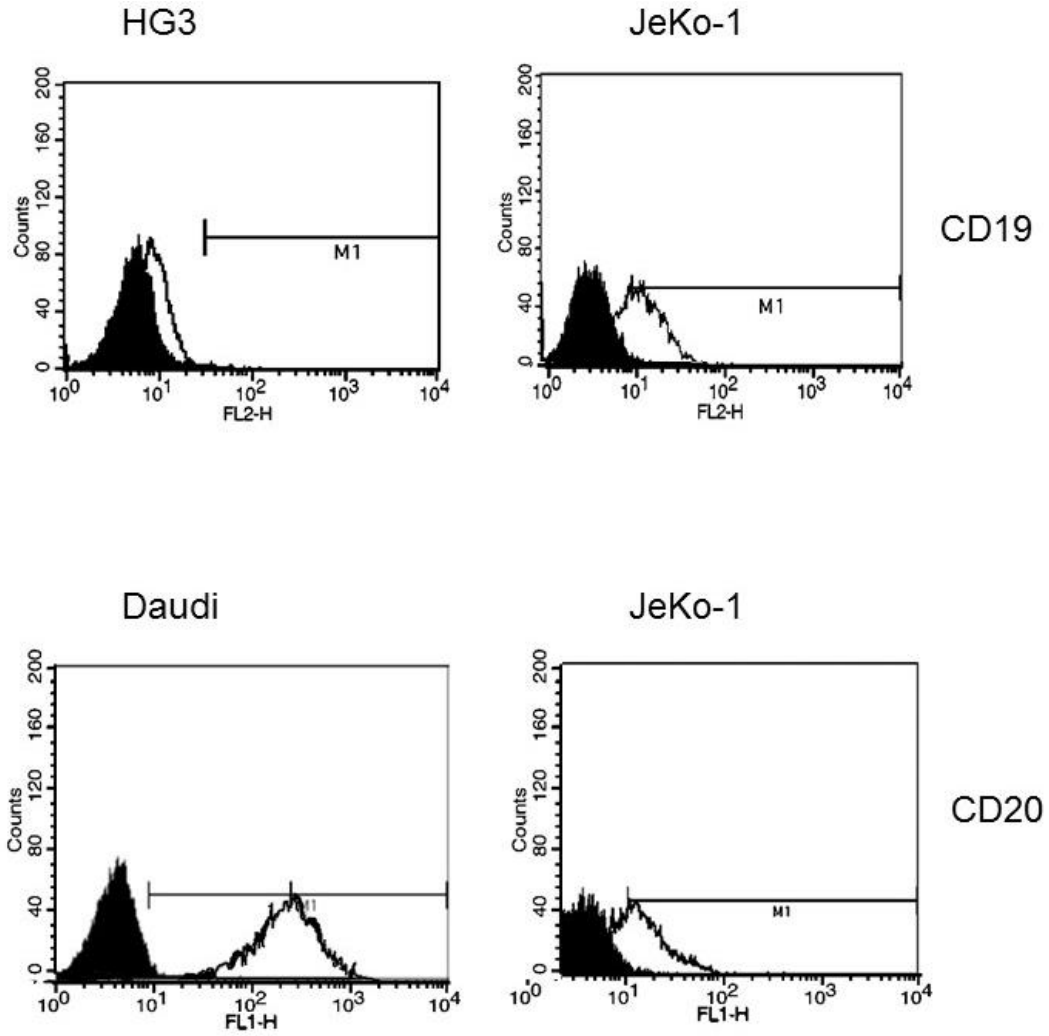


Figure 11: JeKo-1 cells express a sIgM+, CD5+, CD19+, CD20+ immunophenotype similar to a typical CLL clone. JeKo-1 cells were stained with mAbs to detect expression of classic CLL cell markers CD19, CD20, CD5 and sIgM and measured by FACS analysis using a FACSCalibur™ instrument. Primary CLL cells (CLL2134) were used as a comparison for IgM and CD5 expression, and HG3 and Daudi cells were used as positive controls for CD19 and CD20 expression.

3.3.3. Characterization of anti-IgM induced intracellular Ca2+ mobilization

To test calcium mobilization in JeKo-1 and primary CLL cells I used Fluo-4, a cell permeable indicator that increases in fluorescence upon binding released Ca^{2+} (154). A CLL clone, known to be sIgM+ and to respond to BCR crosslinking with calcium flux was used as a positive control. The fluorescence of Fluo-4 loaded cells was initially measured in non-stimulated cells, and then again, following the addition of 20 µg/ml goat $F(ab')_2$ anti–human IgM. A rise in Fluo-4 fluorescence over baseline after BCR crosslinking indicated intracellular calcium release. Figure 12 shows that BCR crosslinking on JeKo-1 cells induced intracellular calcium release. Similarly, such stimulation of primary CLL cells also induced intracellular calcium release, although these latter cells appeared to have a weaker response.

The signalling response of BCR-stimulated JeKo-1 cells, the sensitivity of this response to pharmacological inhibition and immunophenotypic similarity all suggest that these cells can be used to model CLL cell responses. Therefore, I proceeded to use JeKo-1 cells in further experiments involving global phosphoproteomic signalling.

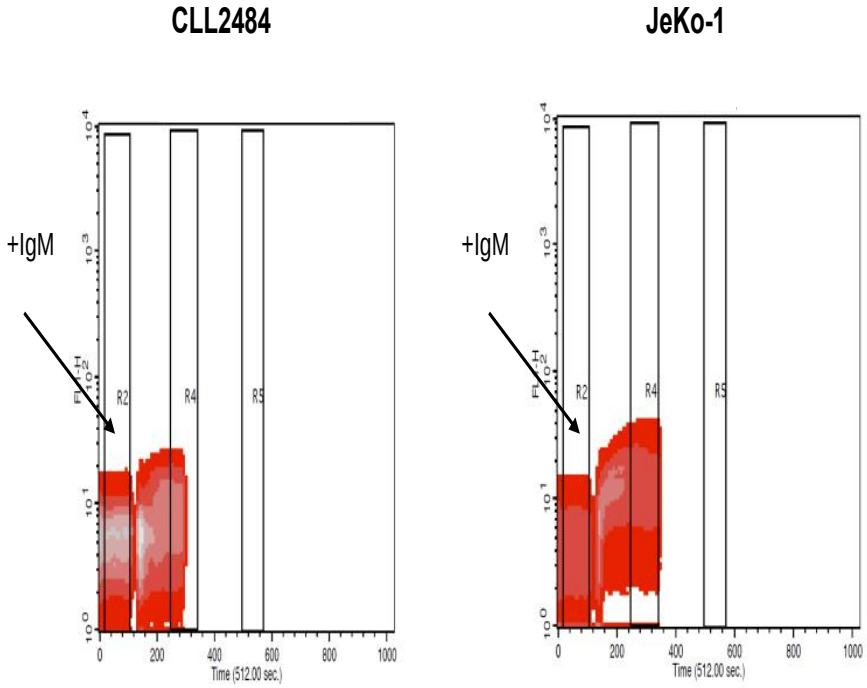


Figure 12: Anti-IgM induced intracellular Ca2+ mobilization in primary CLL and JeKo-1 cells. JeKo-1 cells and and primary CLL cells were labeled with Fluo-4 AM (2 μM). [Ca2+]i was then measured using flow cytometry, taking readings before (baseline) and following anti-IgM (stimulated) treatment to measure changes in fluorescence intensity. The downward arrow indicates the time of anti-IgM addition to the samples (refers to overleaf).

3.3.4. Optimization of BCR crosslinking time and temperature for maximum pY induction in JeKo-1 cells.

BCR signalling depends on the interplay of membrane fluidity, and activation of tyrosine kinases and phosphatases (155). This interplay is both time and temperature dependent (156), and it was therefore necessary to measure these parameters in JeKo-1 cells responding to BCR crosslinking in order to determine the conditions needed for maximum expression of phosphorylated proteins. Figure 13A shows the pattern of pY containing proteins in lysates of

JeKo-1 cells stimulated with anti-IgM at 37°C for various time points. Unstimulated JeKo-1 cells showed low baseline levels of pY and of pERK. Incubation with anti-IgM antibody stimulated an increase in pY and pERK levels, and this increase peaked at 15 minutes before showing a slight decrease at 20 minutes. I next investigated the effect of varying temperature by incubating JeKo-1 cells at 10° C, 20° C and 37° C. This was done to balance the need to stimulate the cells for a certain time period and then preserve the "snap shot" of activation by cooling the cells. Figure 13B shows the results of this experiment. BCR stimulation of JeKo-1 cells at 10°C showed maximal induction of pY, whereas stimulation at 20° C and 37° C showed less. Presumably these differences are because protein tyrosine phosphatases are more active at higher temperatures. However, cells stimulated at 20° C and 37° C showed greater induction of pAkt and pERK than did cells stimulated at 10° C indicating that the BCR signalling pathway was likely intact when cells are stimulated at warmer temperatures. The lower temperature also affects membrane fluidity (See chapter 3.4). Taken together, the data of this section suggests that a temperature of 20°C is optimal bearing in mind that protein tyrosine phosphorylation can be induced that is consistent with other hallmarks of BCR signaling (ie induction of pAkt/pERK).

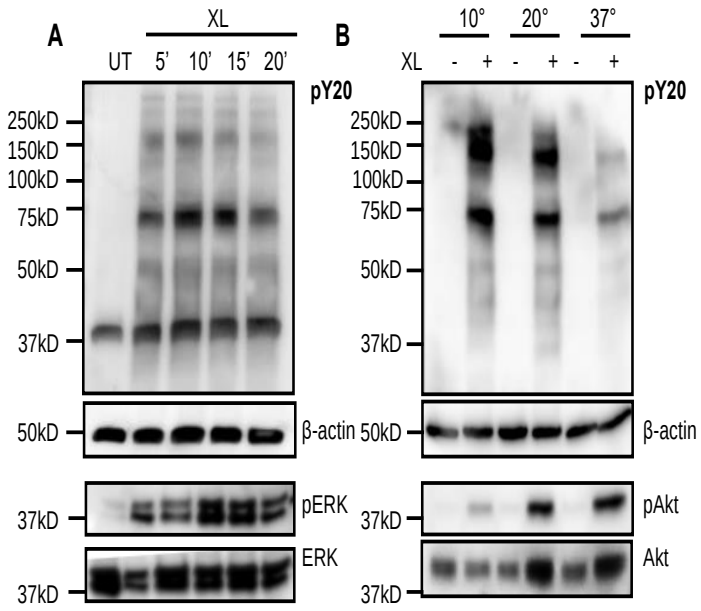


Figure 13: Kinetics of protein tyrosine, Akt and ERK phosphorylation in BCR stimulated JeKo-1 cells at different times and temperatures. A. JeKo-1 cells ($2x10^6$) were serum starved overnight in 24 well plates, and then stimulated with 20 µg/ml $F(ab')_2$ goat anti-human IgM for 5, 10, 15 and 20 minutes at 37° C. B. JeKo-1 cells ($2x10^6$) cultured at 10°C, 20°C and 37°C were stimulated for 15 minutes with anti-IgM. 10 µg of protein derived from cellular lysates was analyzed on a 10% SDS-PAGE gel for the levels of pY (using a pY20 antibody), pAkt and pERK by Western blot. Western blots for β-actin, total Akt and total ERK were used as loading controls. Blots are representative of two independent experiments.

3.3.5. Internalization kinetics of surface IgM in JeKo-1 cells upon BCR stimulation

After having determined the optimal time and temperature parameters to use for the global phosphoproteomics experiment, I decided to monitor internalization of the B-cell receptor under the selected conditions. The internalization of activated receptors by endocytosis has an important role in

regulating the duration and intensity of downstream signalling events. Therefore, I used flow cytometry to look at the levels of BCR on the surface of the JeKo-1 cells at various time points after BCR crosslinking**.** Figure 14 shows surface IgM expression initially increases following BCR crosslinking at 20°C before decreasing at later time points. I found that the 15 min timepoint showed the greatest decrease in expression, corresponding with the greatest degree of pY induction.

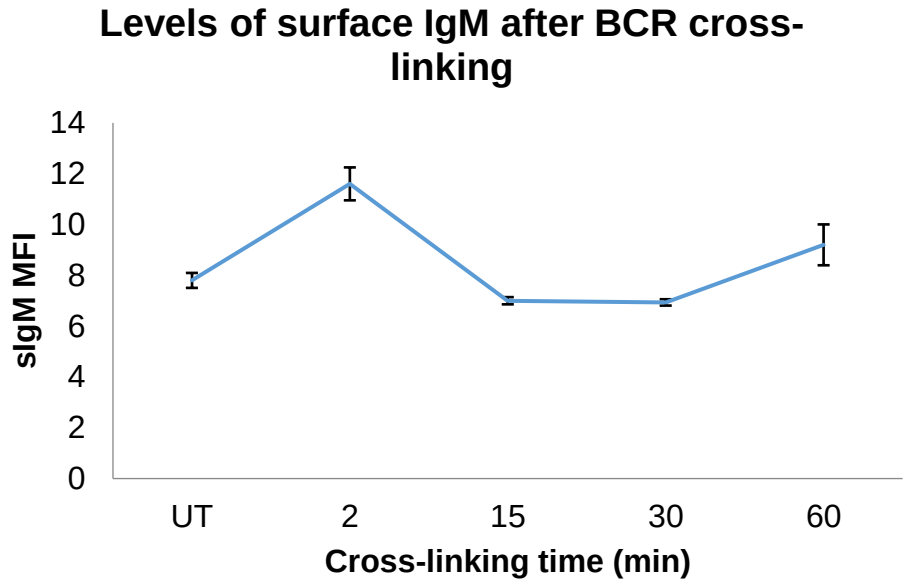


Figure 14: Surface IgM expression in JeKo-1 cells upon BCR stimulation decreases after 15 minutes. At specified times after BCR stimulation, 2× 10^6 JeKo-1 cells were stained with PE conjugated anti-IgM (or isotype control), for 30 minutes in the dark on ice. Cells were washed twice, resuspended in 200 µl FACS buffer, and acquired on a FACSCalibur™ (BD Biosciences, Wiltshire, UK). IgM expression was determined on the gated live cells and mean fluorescence intensity (MFI) was calculated at the different time points.

3.3.6. Antibody titration for pY immunoprecipitation

So far in this thesis analysis of pY proteins was performed at a small scale (2mg of lysate-derived total protein was used). For the proteomics experiment,

greater amounts of protein would be needed, and the initial experimental conditions needed to be optimized in preparation. A titration experiment was performed to determine best antibody: lysate concentration. Determination of this ratio was necessary for this experiment as an excess amount of antibody or proteins within lysates could reduce ultimate yield. In this experiment antibody concentration was changed whereas protein concentration remained constant. Fully concentrated antibodies (c_1) were 1 mg/ml in final lysate solution of 4G10 antibody (Millipore (UK) Ltd, Hertfordshire, UK) (33 µl) and 7 µl of pTyr100. Half-concentrated ($c_1/2$) was 16 µl of 4G10 and 3.5 µl of pTyr100 (New England Biolabs, Hitchin, UK), and quarter concentrated antibody ($c_1/4$) was 7.5 µl of 4G10 and 1.25 µl of pTyr100. Figure 15 shows the results of this titration, comparing the levels of pY proteins within the immunoprecipitates and whole lysates following immunoprecipitation. BCR crosslinking induced protein tyrosine phosphorylation and this was observed in the pre-IP lysates. IP with the fully concentrated antibodies showed maximal immunoprecipitation of pY proteins, and maximal removal of pY proteins from post-IP lysates. The use of half or quarter antibody concentrations showed a step-wise reduction in immunoprecipitated/removed pY proteins (Figure 15). These results indicate that for the purposes of the larger proteomic experiment the maximum amount of antibody (1mg/ml of 4G10 antibody (33µl) and 7µl of pTyr100) should be used.

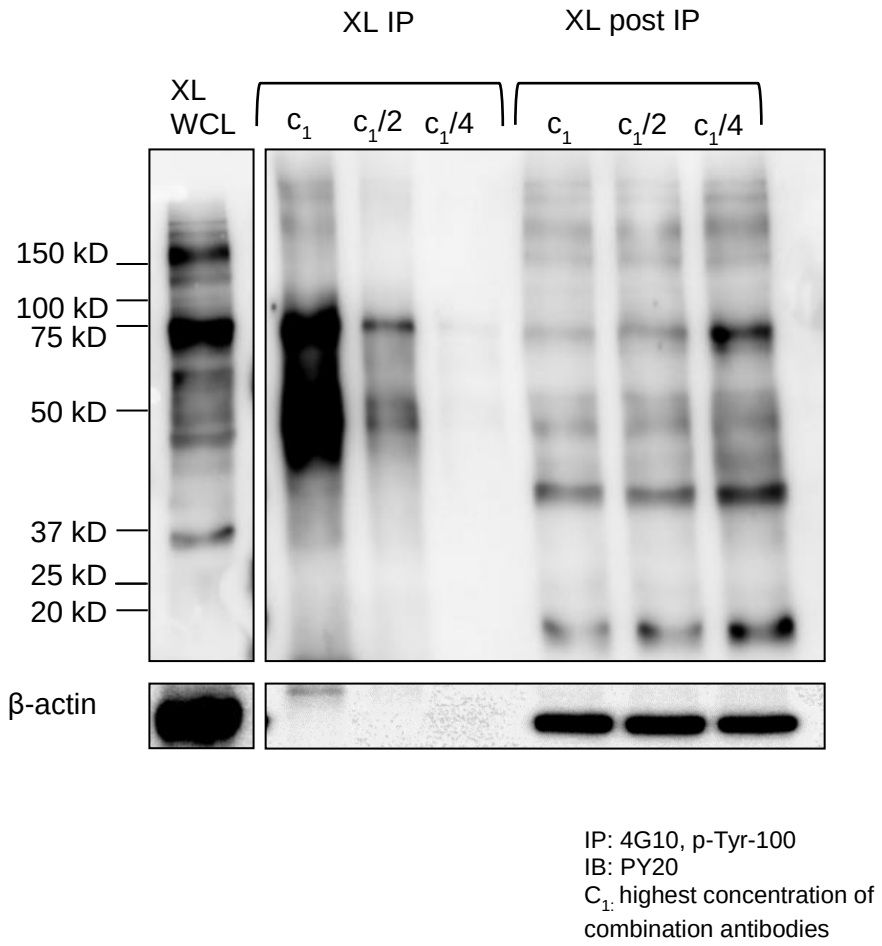


Figure 15: Immunoprecipitation of pTyr network in BCR-stimulated JeKo-1 cells, using a combination of two antiphosphotyrosine antibodies (4G10, p-Tyr-100). JeKo-1 cells were serum starved overnight and stimulated with a $F(ab')_2$ goat anti-human IgM at 20°C on the following day. Following 6 hours of immunoprecipitation with a combination of anti-phosphotyrosine antibodies (4G10, p-Tyr-100) in titrated concentrations (c_1, $c_1/2$, $c_1/4$), cellular lysates were analysed by SDS-PAGE. Detection was performed using a second anti-phosphotyrosine antibody (pY20, Santa Cruz Biotechnology, Inc, Heidelberg, Germany), β-actin is used as a loading control.

3.4. Discussion

The aim of this chapter was to identify a B-cell line to use as a BCR signalling model for CLL cells. I found that JeKo-1 cells seemed to be a good model based on their surface phenotype, response to BCR crosslinking and sensitivity of this response to pharmacological inhibitors. Further investigation of this cell line showed good induction of protein tyrosine phosphorylation that would be useful for analysis of global signalling in the next chapter.

In terms of the signalling properties of the candidate B cell lines, I used the criterion of phosphorylation of ERK and Akt as markers of BCR activation. According to my results, HG3 and MEC-1 cells, cell lines derived from primary CLL cells (141,145) that are considered to be good models of CLL cell behaviour when used in *in vivo* studies showed high basal levels of pERK and pAkt. This finding allowed me to reject these CLL cell lines in favour of JeKo-1. Similarly, Raji and Daudi cells, cell lines derived from Burkitt's lymphoma cells, could also be rejected because of constitutively high basal levels of pERK or pAkt respectively. The presence of high basal levels of pERK and/or pAkt indicate the presence of intracellular signals which may confuse subsequent analysis of the phosphoproteome, performed in a subsequent chapter. This is why HG3, MEC1, Raji and Daudi cells could be rejected.

When stimulated with anti-IgM JeKo-1 cells responded with strong induction of intracellular calcium flux, phosphorylation of ERK and Akt and protein tyrosine phosphorylation. With respect to induction of pERK and pAkt, the results we generated with JeKo-1 cells were similar to those generated with A20 cells, a mouse cell line derived from murine B-lymphocytes. JeKo-1 cells were again chosen in favour of A20 cells because of phenotypic similarity with primary CLL cells. JeKo-1 cells are CD5 positive and express IgM as their BCR.In contrast; A20 cells are negative for CD5 and express IgG as their BCR. Primary CLL cells are typically CD5/IgM positive. IgM and IgG BCRs have fundamentally different signalling outputs; the former promoting survival and proliferation, whereas the latter promotes plasmacytic differentiation (60)

Another aspect related to CLL signalling that I used as a decisive factor for this model was response to pharmacological inhibitors. Several inhibitors targeting the BCR have emerged in recent years, and a role for these inhibitors in the treatment of patients with chronic lymphocytic leukemia and other B-cell malignancies is under investigation (37,157). Previous work from this lab showed a principle role for the SFK Lck in mediating proximal and distal signalling events in CLL cells responding to BCR stimulation, and that these cells were sensitive to the Lck inhibitor 4-amino-5-(4-phenoxyphenyl)-7H-pyrrolo[3,2d] pyrimidin-7-yl-cyclopentane (150). I tested the candidate cell lines to investigate their sensitivity to Lck inhibition, JeKo-1 cells showed partial response with respect to inhibited induction of pAkt, pERK and pSyk whereas A20 cells showed only inhibited induction of pERK. Thus, JeKo-1 cells appeared more similar to CLL than A20 cells with respect to their sensitivity to Lck inhibition.

In conclusion, I decided to use the mantle cell lymphoma cell line JeKo-1 as a model for my studies of CLL phosphoproteomic signalling. This cell line has been previously used to look at phosphoproteomic analysis of mantle cell lymphoma cells, and this has highlighted the importance of BCR signalling in MCL (158). Further experiments showed that maximum pY induction in BCR stimulated JeKo-1 cells occurs at 20°C after approximately 15 minutes of BCR crosslinking. The selected temperature showed some limitations as it is known that lowering temperature affects membrane fluidity (159). Perturbation of membrane fluidity can impact cellular signalling (160), however using a lower temperature allowed me to be able to control duration of signalling in my proteomics experimental set up and the data in this chapter suggest that certain pathways were not affected by the choice of the 20°C temperature. I was also able to establish optimal immunoprecipitation conditions to achieve good pull-down efficiency for tyrosine phosphorylated proteins and their co-associated network.

4. Chapter – Phosphoproteomic analysis of BCR signalling.

BCR-associated studies have grown exponentially over the past decade particularly those involving signalling because of the role BCR signalling plays in B-lymphoid malignancy (148,161,162). At the beginning of this study, mostly targeted approaches based on preconceived hypotheses were used. These approaches often focused on the role of single elements within the BCR signalling pathway. While these studies were useful for constructing basic understanding of this pathway, they gave no information on how this pathway functions in different B-cell subtypes or how this pathway is subverted in the pathogenesis of B-cell lymphomas.

The focus of this thesis was to gain insight into BCR signalling in primary CLL cells because of the role this pathway plays in the pathogenesis of this disease. The results of the previous chapter identified JeKo-1 cells as a potential cell line to model our understanding of BCR signalling in primary CLL cells. The aim of this chapter was to perform a hypothesis-free discovery proteomics approach to characterize the BCR signalling pathway in JeKo-1 cells. Based on a method developed by Matthias Mann (163), we used antiphosphotyrosine antibodies to pull down tyrosine phosphorylated proteins and their co-associated network from resting and BCR-stimulated JeKo-1 cells. Differentiation between these two activation states of JeKo-1 cells was achieved using SILAC technology (139) where the proteins derived from the activation states could be identified by LC/MS based on isotopic differences of select amino acids used to label the cells. Following the MS analysis different databases and web resources were used to assemble the BCR signalling pathway and look for potential protein-protein interactions.

With regards to the chosen proteomics approach, an important parameter in the analysis of tyrosine phosphorylation by mass spectrometry has been the development of pTyr-specific antibodies. At present, different antibodies such as 4G10, pY20, pTyr100, pY99 and pT66, have been used to enrich pTyr

proteins for MS analysis (164). The basis of this study was the work of Matthias Manns's group who chose to use a mixture of pTyr100 and 4G10 to look at protein phosphorylation in a time-course study of activation following epidermal growth factor stimulation (163). Antibody selection is an important factor for these experiments as the SILAC ratio of a protein is essentially a measure of the differences in the protein's affinity (directly or indirectly through a binding partner) towards the anti-pTyr antibody before and after BCR crosslinking. Different studies have been published evaluating performance of different anti-phosphotyrosine antibodies in terms of their specificity and sensitivity (165,166). Anti-phosphotyrosine antibodies binding to tyrosine-phosphorylated peptides exhibit substantial sequence selectivity. Michele Tinti et al. demonstrated that different phosphotyrosine antibody clones recognized their target sites in a sequence-specific manner, and that this differed between clones. According to peptide microarray data, different clones exhibit differences between the sequence preferences and these specificity differences can be reflected in Western blots, where band intensities of 4G10 and p-Tyr-100 differed and pY20 even stained an additional group of proteins (166).In the Blagoev study as well as a number of others a mixture of individual anti-phosphotyrosine monoclonals was used to improve pull-down coverage (167).

One of the advantages of pTyr enrichment at the protein level that is central to this study is that pTyr protein binding partners can be identified and provide information on phosphorylation-dependent protein–protein interactions. Results from the quantitative analysis can be used to discriminate the true binding partners from the nonspecific bindings by looking at the SILAC ratio. It should also be noted that the protein–protein interactions that specifically rely on phosphorylated tyrosines, such as those mediated by SH2 domains, are sometimes not present in the IP due to competitive binding from the antibody with proteins carrying these domains for a given pTyr protein target (168). Another possible limitation is that when any nonspecific binding proteins that are introduced during sample preparation (e.g keratins) are overly abundant they will reduce the analytical space of LC-MS/MS and therefore decrease the ability to identify target proteins.

The results of the proteomic studies in this chapter included some of the well-known components of active BCR signalling (22), thus validating my strategy. This work also highlighted the presence of actin reorganization components in the active proteome, and, in particular, members of the Arp2/3 complex that had not been previously studied in a B-cell setting. Thus, I identified ARPC5L within the signalling complex of stimulated JeKo-1 cells.

4.1. Materials and methods

4.1.1. SILAC labelling

JeKo-1 cells were cultured in media containing either SILAC light lysine and arginine (labelled with natural isotopes - Lys0, Arg0) (Sigma-Aldrich Company Ltd, Dorset, UK) or SILAC heavy lysine or arginine (labelled with heavier isotopes - Lys8, Arg10) (CK Isotopes, Ibstock, UK). To ensure the added amino acids are the sole source of nutrients we used dialyzed serum (MWCO 10000 Da, Dundee Cell Products, Dundee, UK) in the culture media (139). An excess amount of proline is also added to the formulation to prevent arginine to proline conversion (169) (Table 6).

Heavy SILAC medium	Light SILAC medium		
		Mass difference	Concentration in RPMI
L-Arginine: HCL ($^{13}C_6{}^{15}N_4$), **Arg10**	L-Arginine, **Arg0**	10 Da	84mg/l
L-Lysine: 2HCL ($^{13}C_6{}^{15}N_2$), **Lys8**	L-Lysine monohydrochloride, **Lysine0**	8 Da	146mg/l
L-Proline	L-Proline	-	200mg/l

Table 6: Components for SILAC heavy and light medium. Aminoacids for Heavy SILAC medium were purchased from CK Isotopes (Ibstock, UK). Aminoacids for Light SILAC medium were purchased from Sigma-Aldrich Company Ltd, Dorset, UK.

4.1.2. SILAC labelling efficiency

To test incorporation of SILAC amino acids in the JeKo-1 cell proteome, cells were cultured in SILAC light or heavy medium for 8 population doublings. The cells were then lysed (for lysis conditions see chapter 4.2), and 50 μg of protein within these lysates was separated by SDS-PAGE using a NuPAGE™ Novex™ 4-12% Bis-Tris Protein Gel (Life Technologies Ltd, Paisley, United Kingdom). Following Coomassie blue staining/destaining, the corresponding large band from each lane was excised, digested with trypsin and the peptides analysed by MS in a single run. Analysis of the raw files in order to determine the ratio of heavy/light labelled peptides was performed using MaxQuant software (170), and incorporation efficiency was calculated as: (1-1/Ratio(H/L)) on the peptide level. In our experiment, Jeko-1 cells were tested for both Arginine and Lysine incorporation, and labelling efficiency was determined to be higher than 98%.

4.1.3. Sample preparation for mass spectrometry

Proteins within cell lysates were separated by SDS PAGE using a NuPAGE™ Novex™ 4-12% Bis-Tris Protein Gel (Life Technologies Ltd, Paisley, United Kingdom). Gels were run using 200 V constant voltage for 50 min, or until the dye front exited the gel. The gel was stained with a Colloidal Blue Staining Kit, (Life Technologies Ltd, United Kingdom) according to the manufacturer's instructions, and then destained with dH_20. At this point we scanned the gel in order to mark the bands that we planned to excise. The bands of interest were excised with sterile scalpels (Swann-Morton, UK), and then sliced into smaller pieces that were placed in protein Eppendorf™ LoBind Microcentrifuge Tubes **(**Life Technologies Ltd, Paisley, UK). The band pieces were then washed for 15 min with dH_20, then with acetonitrile (Life Technologies Ltd, Paisley, UK) and finally the pieces were washed again with dH_20, Ammonium bicarbonate 100mM solution (Sigma-Aldrich Company Ltd, Dorset, UK) was added and the samples were incubated for 15 min, followed by further incubation with 50mM ammonium bicarbonate /50% acetonitrile solution at 37°C in order to destain the gel slices. An Eppendorf ThermoMixer®, (Eppendorf, UK) set to 900 rpm was used to facilitate destaining until the blue color was removed. The gel pieces were dehydrated by first washing them with 100 µl of acetonitrile and then drying the gel pieces in an Eppendorf™ Speed Vac (Fisher Scientific UK Ltd, Leicestershire) for 5 min.

In the next step of sample preparation disulphide bridges in the peptides were reduced. This was done by incubating the gel slices in 50 µl of 10 mM DTT in 100 mM Ammonium bicarbonate in a thermoshaker at 56°C for 1 h. Following this reduction step, the samples were alkylated by adding 50 µl of 50mM iodoacetamide in 100 mM ammonium bicarbonate and incubating them for 30 min at RT in the dark. The gel pieces where then washed in two steps: First using 100 mM ammonium bicarbonate and shaking at 900 rpm for 15 min and then using 20 mM ammonium bicarbonate/acetonitrile (50:50v/v) keeping the

same conditions. After the washes the pieces were then dehydrated with acetonitrile and dried in the SpeedVacuum as described above.

After the reduction/alkylation step, Trypsin Gold (Promega, UK) diluted in reaction buffer (40mM ammonium bicarbonate, 9 % acetonitrile) was used to digest the band pieces at a 1:25 trypsin:protein ratio (0.5 µg of trypsin per band) for 30 min to rehydrate the gels which were then further incubated at 30°C overnight.

Finally, digested peptides were extracted from gel slices with formic acid (Fluka, VWR International Ltd, West Sussex, UK). Gel slices and formic acid were then transferred to a fresh eppendorf tube and then centrifuged at full speed (14000xg) for 15 min. The supernatant was taken, placed into a fresh protein Eppendorf™ LoBind Microcentrifuge Tube and placed in a SpeedVac concentrator at 65°C to dry down. The pellet containing the peptides was resuspended in 1% formic acid.

4.2. Immunoprecipitation of tyrosine phosphorylated proteins and their co-associated network from BCR-stimulated JeKo-1 cells (large scale)

JeKo-1 cells were labelled with heavy and light SILAC medium in large T175 flasks (Corning®, Sigma Aldrich, Dorset, UK) as described above, to obtain a minimum of $5x10^7$ JeKo-1 cells per condition. The cells were washed with PBS, and the culture medium was replaced with respective serum free SILAC medium and left overnight in standard culture conditions. On the next day, the heavy labelled cells were treated with 20 µg/mL of $F(ab')_2$ goat anti-human IgM for 15 min at RT to stimulate the BCR, while light labelled cells were incubated under the same conditions but were left unstimulated. Following stimulation both heavy and light labelled cells were transferred to ice-chilled Falcon tubes and placed in an ice bath to stop signalling. The JeKo-1 cells were then centrifuged at 500 rcf at 4° C for 5 min, and washed 1x with cold PBS. The cells were lysed with 15 ml of ice cold lysis buffer (Table 7) and left on ice for

15 min. Insoluble material was removed by centrifugation. A protein assay was performed on the supernatant (Chapter 2.3.2) and 200 µg of protein from each lysate were saved to perform validation Western blotting experiments.

The rest of the lysates from heavy and light labelled cells were mixed in a 1:1 ratio using 20 mg of each. To start the immunoprecipitation process, the lysates were initially precleared with 1 ml of protein A agarose beads (Calbiochem®, Millipore U.K. Limited, Hertfordshire) for 1 hour at 4°C with rotation. These beads were removed by centrifugation at 4000 rpm for 5 min, and the supernatant further incubated with 1mg of anti-phosphotyrosine, clone 4G10®, agarose conjugate antibody (Millipore, UK) for 2 hours at 4°C with rotation. This followed by the addition of 400 µl of anti-phosphotyrosine P-Tyr100 mAb conjugated sepharose (NewEngland Biolabs, Hitchin, UK) and incubation for an additional 4 h at 4° C with rotation. After a total of six hours, the limmunoprecipitates were washed in lysis buffer (Table 7) by centrifugation for 5 min at 500 rpm and precipitated proteins eluted with the addition of 2 ml of 0.1M glycine (pH 2.4) incubation for 3 min with rotation at 4°C and centrifugation 500 rpm for five min. This elution procedure was repeated twice more, saving the supernatant each time. Acidity within the collected elution supernatants was neutralized with neutralization buffer (Table 7). At this point, Centricon® Plus-70 Centrifugal Filter Units (Millipore (U.K.) Limited, Hertfordshire, UK) with a 10 kDa cutoff were used to concentrate proteins within the supernatants by spinning three times (for 30 min, 10 min, 5 min) at 3000 g at 4°C. Sample volume within concentrates was further reduced to approximately 25 µl using a SpeedVac concentrator (Life Technologies Ltd**,** Paisley, UK). Proteins within the prepared sample were separated by SDS-PAGE as described above Following Colloidal Blue staining and destaining (Novex™, Fisher Scientific - UK Ltd**,** Loughborough), protein bands were excised and digested and prepared for MS as described above (Chapter 4.1.3).

Lysis buffer		

Components	Concentration	Supplier
Tris-Cl (pH 7.4)	20mM	Sigma-Aldrich Company Ltd, Dorset, UK
NaCl	150 mM	Fisher Scientific UK Ltd, Loughborough
β-Glycerophosphate	40 mM	
NaF	10 mM	Sigma-Aldrich Company Ltd, Dorset, UK
IGEPAL®	1%	Fisher Scientific UK Ltd, Loughborough
Sodium deoxycholate	0.1%	Fisher Scientific UK Ltd, Loughborough
Protease inhibitor, cocktail set V, EDTA free	1:50	Millipore (U.K.) Limited, Hertfordshire
Phosphatase inhibitor, cocktail set III, EDTA-free	1:50	Millipore (U.K.) Limited, Hertfordshire

Neutralization buffer		
Components	**Concentration**	**Supplier**
Tris-Cl (pH 8)	2 M	Sigma-Aldrich Company Ltd, Dorset, UK
NaCl	1.5 M	Sigma-Aldrich Company Ltd, Dorset, UK
EDTA	1 mM	

Table 7: Buffer components for lysis and neutralization buffer for proteomics immunoprecipitation experiment.

4.3. LC−MS/MS and Data Processing

Five microliters of prepared peptide samples from potein bands was mixed with 15 ul of 0.5% formic acid (Fluka, VWR International Ltd, West Sussex, UK), and then fractionated by nanoscale C18 high performance liquid chromatography (HPLC) on a Waters nanoACQUITY UPLC system coupled to an LTQ- OrbitrapXL™ mass spectrometer (Thermoscientific, Life Technologies Ltd, Paisley, UK). Peptides were loaded onto a 5 cm ×180 μm trap column (BEH-C18 Symmetry; Waters Corporation) in 0.1% formic acid according to (171).

The generated raw MS peak list was searched against a decoy IPI-human database using the MASCOT search engine. The raw MS files were also processed with the MaxQuant software using the following settings: The minimum required peptide length was set to 6 amino acids and two missed cleavages were allowed. The results of the database search were further processed and statistically evaluated by MaxQuant. The false discovery rate (FDR) for both the peptides and proteins was set to 0.01 to ensure that the worst estimate a hit had a probability of 1% of being a false identification. Proteins with at least one peptide unique to the protein sequence were considered as accepted identifications. For protein quantitation in the pTyr data set, only proteins with at least three peptides (one unique) were selected. SILAC ratios were considered to be significantly changed if at least a 1.5-fold increase/decrease was observed. Microsoft Excel™ was used to arrange the data in order of number of peptides, and to remove the entries for proteins lacking more than one peptide. Peptide data was also sorted by SILAC ratio (H/L), and finally, quantitated SILAC ratios were converted to $\log_2$ values.

4.4. siRNA mediated knockdown of ARPC5 paralog expression

For the purposes of this thesis siRNA was used to achieve transient knockdown of ARPC5A and L in cell lines. Table 8 lists the siRNA oligonucleotides used for these transient knockdowns, including the negative control (scrambled) siRNA oligonucleotide. In general, the siRNA oligonucleotides were used as a pool of 4 for each target (ON-TARGETplus®, Dharmacon, Thermoscientific UK) to target the genes of interest. siRNA pools or single oligonucleotides were resuspended in 1x siRNA buffer to a stock concentration of 20 μM. Aliquots of 2 μM were prepared to avoid freeze-thaw degradation. The final concentration of the siRNA oligonucleotide pool for each experiment was 40 nM.

For transfection of MCF7, cells were seeded at $0.54x10^6$ cells/dish (Costar®, Sigma-Aldrich Company Ltd., Gillingham, UK) 6 cm dishes and left overnight under normal culture conditions. The following day the cells were used if they reached approximately 60% confluency.

To prepare the transfection reagent, Oligofectamine™Reagent (Fisher Scientific UK Ltd, Paisley) diluted in Opti-MEM® (Fisher Scientific, UK Ltd, Paisley) was mixed with siRNA and left on ice for 20 min. In the meantime, supernatant DMEM was removed from MCF7 cell cultures, and the wells were washed with PBS. To complete the transfection procedure, antibiotic-free DMEM media was added followed by the oligofectamine/siRNA mix. The cells were incubated overnight; the supernatant was aspirated gently and replaced with fresh antibiotic–free media containing no siRNA. The cells were cultured for another 48 hours under normal conditions, to be used in further experimentation.

4.5. Results

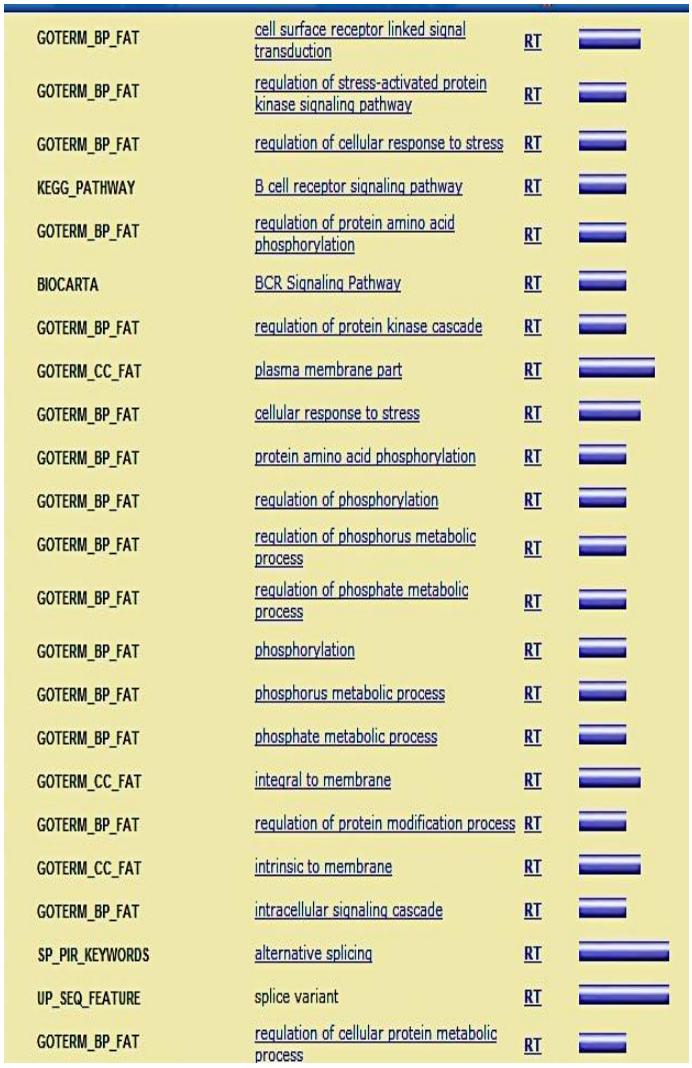
4.5.1. BCR responsive proteins

This proteomic experiment identified a total of 854 proteins within the anti-pTyr immunoprecipitate from BCR-stimulated and unstimulated JeKo-1 cells (Supplementary Table 1, Supporting information). 1.41 (log2=0.5) was chosen as a threshold for a significant ratio change because this could be used to rule out proteins found in a mixture of labelled and unlabelled cell lysates which would be expected to be present at a ratio of 1:1. Using this cut-off 60 proteins were defined as being responsive to BCR stimulation (Figure 16); 35 proteins were found to be “up regulated” (more abundant in pY IP) upon stimulation and 25 were “down regulated” (less abundant in pY IP). In the next section, I used different software packages to visualize the results and map networks and pathways within this dataset.

Figure 16: Sixty proteins in the phosphotyrosine network of stimulated JeKo-1 cells were found to be BCR responsive. Diagram illustrating the distribution of the sets of peptides identified by antiphosphotyrosine immunoprecipitation in JeKo-1 cells. 35 proteins were significantly upregulated and 25 proteins downregulated (fold change>1.5) after stimulation of the BCR with goat F(ab')2 Anti-Human IgM for 15 min.

4.5.2. Functional annotation analysis of overrepresented proteins in BCR active network using software DAVID

Database for Annotation, Visualization, and Integrated Discovery (DAVID) is a web-based functional annotation tool that allows comparison of the 35 proteins responsive to BCR stimulation within the full network of immunoprecipitated proteins (172). DAVID uses public genomic resources (e.g. NCBI, PIR, SWISS-PROT, GO, OMIM, PubMed, KEGG) to perform functional annotation of the “enriched” clusters to give biological meaning to our data. According to the functional annotation list generated by DAVID, (Figure 17) the shortlisted proteins that stand out from the pTyr network when the BCR is crosslinked are grouped in functional clusters that are related to BCR signalling. The clear over-representation of BCR signalling pathways in our data is solid evidence of the efficiency and specificity of our method.



GOTERM_BP_FAT	cell surface receptor linked signal transduction	RT	
GOTERM_BP_FAT	regulation of stress-activated protein kinase signaling pathway	RT	
GOTERM_BP_FAT	regulation of cellular response to stress	RT	
KEGG_PATHWAY	B cell receptor signaling pathway	RT	
GOTERM_BP_FAT	regulation of protein amino acid phosphorylation	RT	
BIOCARTA	BCR Signaling Pathway	RT	
GOTERM_BP_FAT	regulation of protein kinase cascade	RT	
GOTERM_CC_FAT	plasma membrane part	RT	
GOTERM_BP_FAT	cellular response to stress	RT	
GOTERM_BP_FAT	protein amino acid phosphorylation	RT	
GOTERM_BP_FAT	regulation of phosphorylation	RT	
GOTERM_BP_FAT	regulation of phosphorus metabolic process	RT	
GOTERM_BP_FAT	regulation of phosphate metabolic process	RT	
GOTERM_BP_FAT	phosphorylation	RT	
GOTERM_BP_FAT	phosphorus metabolic process	RT	
GOTERM_BP_FAT	phosphate metabolic process	RT	
GOTERM_CC_FAT	integral to membrane	RT	
GOTERM_BP_FAT	regulation of protein modification process	RT	
GOTERM_CC_FAT	intrinsic to membrane	RT	
GOTERM_BP_FAT	intracellular signaling cascade	RT	
SP_PIR_KEYWORDS	alternative splicing	RT	
UP_SEQ_FEATURE	splice variant	RT	
GOTERM_BP_FAT	regulation of cellular protein metabolic process	RT	

Figure 17: Functional annotation of enriched Gene Categories and Pathways estimated by DAVID Bioinformatic Tools. Chart Report listing GO enrichment for overrepresented proteins in the BCR network, using whole human genome as reference background, confirms the overrepresentation of BCR signalling (p value less than 0.0001). RT: Related term search (bar indicating number of genes involved in each term).

4.5.3. Protein class analysis using Panther software

PANTHER (Protein ANalysis THrough Evolutionary Relationships) allowed me to analyze the list of proteins that I found to be enriched in this dataset, and classify them based on molecular function, biological process, cellular

component or pathway (173). This program is useful for understanding protein functionality within a network of proteins. PANTHER groups proteins based on class and visualizes the results in the form of a pie chart. According to the output generated by the BCR crosslinking experiment, the most represented protein class in my data is cytoskeletal proteins (Figure 18). This finding suggests an important role for actin related proteins in BCR signalling, and it lead me to focus on this particular group of proteins.

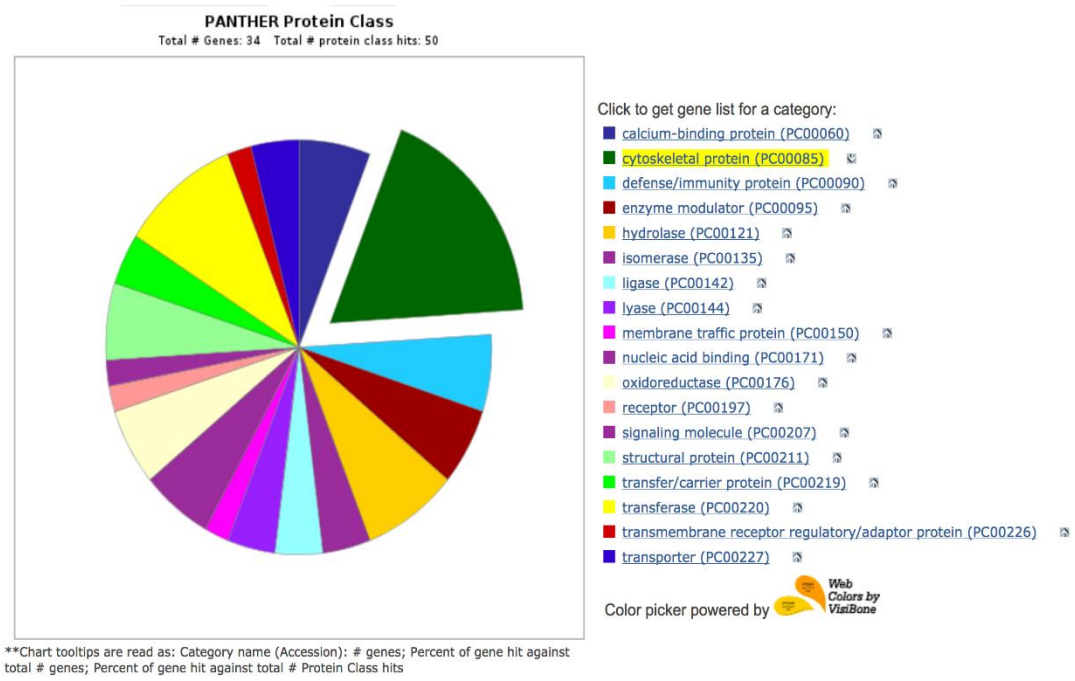


Figure 18: Protein classes of the 60 proteins with altered expression in JeKo-1 cells, upon BCR stimulation, according to PANTHER classification. A pie chart of the 21 protein classes assigned by PANTHER to categorize the BCR-responsive proteins highlights the role of cytoskeletal proteins within our dataset.

4.5.4. STRING network

Finally, to visualize the full list of 35 proteins significantly increased in response to BCR signalling within the pTyr network I used STRING to construct a protein

interaction network. STRING imports data from experimentally derived protein–protein interactions through literature searches, from interactions computed from genomic features and from interactions inferred from model organisms based on orthology to form predicted interaction networks (174). In the discovery proteomics experiment I used STRING to map possible connections between overrepresented proteins and then used this map as a screening tool to identify novel targets. The output produced by this resource is a network of coloured nodes. The nodes represent the protein input (the different colours are a visual aid and do not have any relevance to the specific proteins). At each node, there are icons inside the protein spheres, these icons do not have any particular meaning other than that there is a structure associated with them. This can be either a Protein Data Bank entry for the protein itself or a close homolog. In terms of the size of the nodes, a small bubble (without icon) means that there is no structural information available. With regards to the different coloured lines connecting the nodes: these can either signify known interactions from interaction databases (blue) and curated experimental data (pink) or computationally predicted Interactions because of co-expression (black) and protein homology (purple).

According to the STRING output (Figure 19) the results seem to group into three major interconnecting clusters: A central cluster that mirrors early BCR proximal activation events, which require and involve the BCR itself. Thus, I found CD79B, Lyn, Syk, PLCγ2 and GAB1 within this central cluster. With regards to the kinase Syk, this was the most prominently overrepresented protein within my dataset and had a fold increase of 10.19. Lyn was the ninth most prominently overrepresented protein within the dataset with a fold increase of 2.23. I found a second cluster that points to BCR-antigen internalization and processing events (MHC class II), and a third cluster that is related to cytoskeletal reorganization. Within this cytoskeletal cluster I observed a connection with three proteins (ARPC5L, ARPC2 and Arp3) that belong to the ARP2/3 complex, and found further that if the fold change threshold was lowered from 1.41 to 1.2 five out of seven subunits of the Arp2/3 complex appeared in the data (Arp2, ARPC4). Importantly, identification of ARPC5L which has a 3.74 fold increase upon crosslinking and is connected

to other members of the ARP2/3 complex is a novel find in connection with B cells. The total number of ARPC5L distinct peptide sequences identified in my dataset is 2. (Supplementary Table 1) Taken together this data confirms several aspects of known components within the BCR signalling pathway, and further identifies novel components.

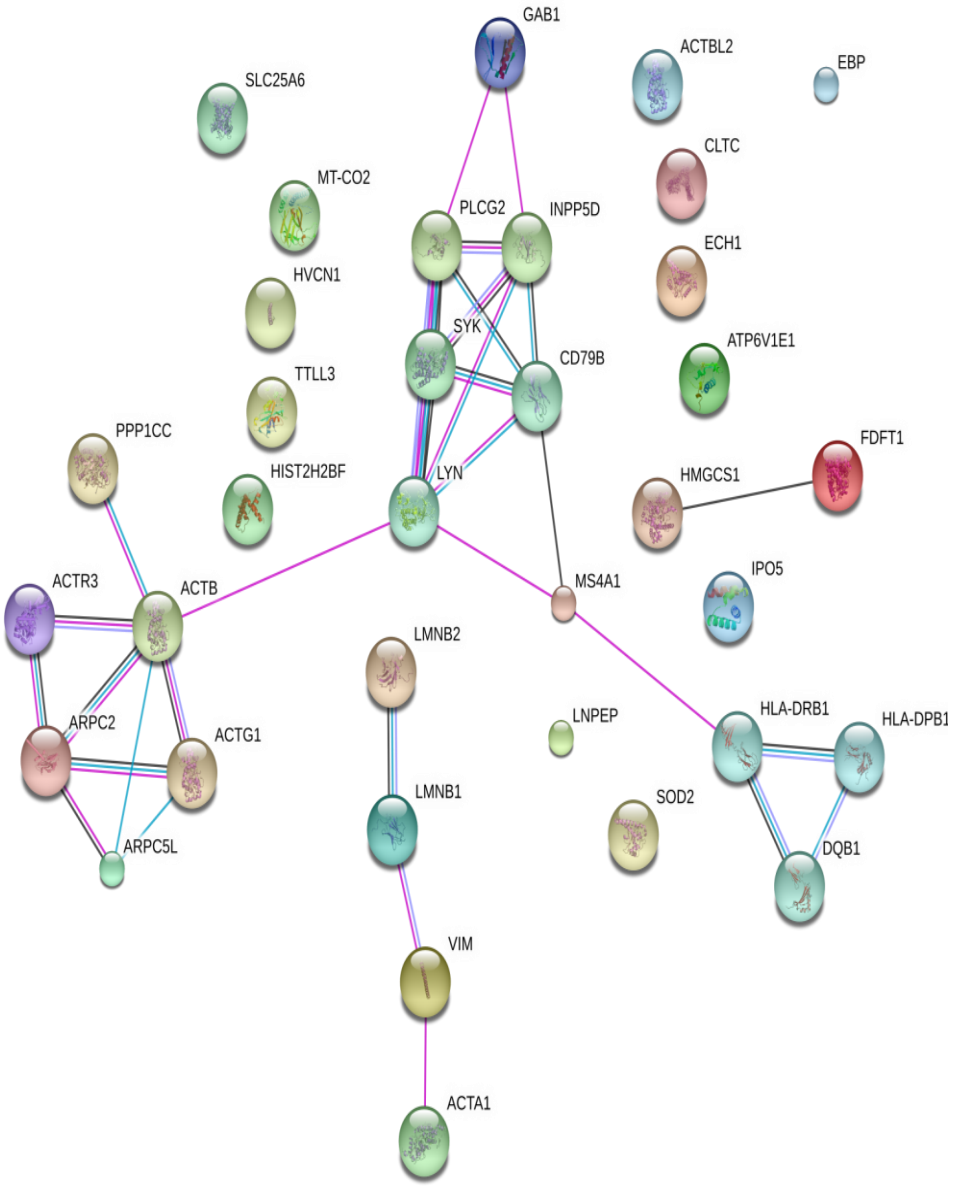


Figure 19: Global snapshot of BCR signaling in JeKo-1 cells following 15min of stimulation.Protein interaction networks of the BCR pTyr network, analysed by STRING include ARPC5L linked with other members of the Arp2/3 complex. The edges that connect the network nodes represent protein-protein associations according to the following specifications: For known interactions 1) from curated databases , 2) experimentally determined . For interactions because of 1) co-expression and 2) protein homology .

4.6. Proteomics validation experiments

4.6.1. Technical replicate

To establish the variability of the mass spectrometry analysis (instrumental error) I performed a technical replicate of the proteomics experiment. This was done by re-analysing the same peptide samples, using the same instrument parameters and then comparing the protein lists from each MS run. Figure 20 shows the results of my findings. 27% less protein identities were included in the technical replicate run (peptides observed in both runs are depicted in black whereas those found in a single run in grey), variation that can be attributed to peptide ions that have quantitation values near the detection limit and therefore do not appear in every replicate run (175). However, the “BCR signature” proteins are present in the technical replicate dataset, as well as 15/35 proteins from the BCR stimulation responsive overrepresented group, Indicatively, Syk and Vim are the two proteins with the highest Heavy/Light ratio in both the original experiment and the replicate, other proteins such as CD79B and LMNB1 are present in both runs (Supplementary Table 2, Supporting information). On the other hand ARPC5L was only identified once in the initial experiment but was absent from the technical replicate. This could be because the protein has a small size (153 aminoacids) and contains fewer tryptic sites so it is harder to identify.

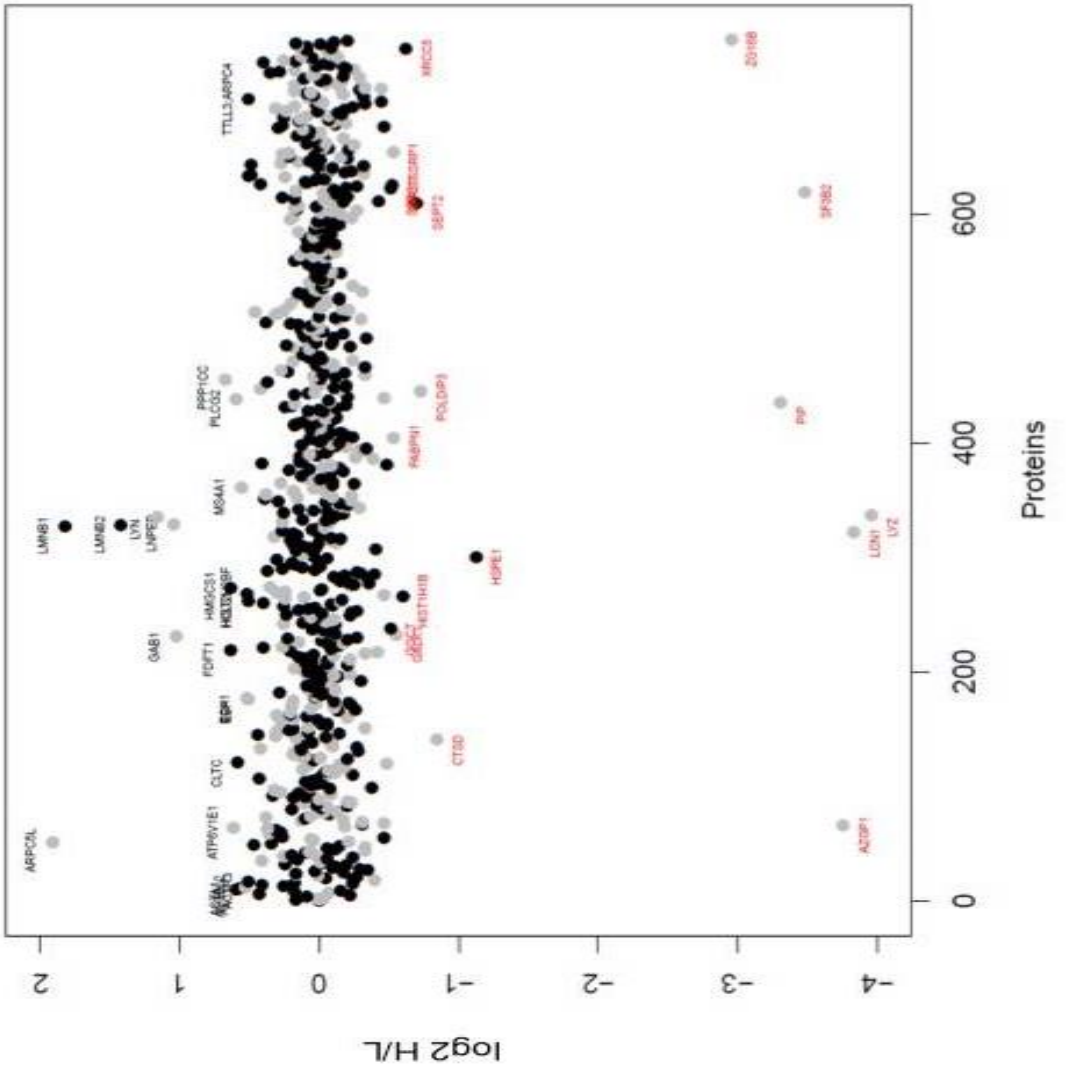


Figure 20: Evaluation of technical reproducibility of mass spectrometry analysis.Scatter plots of log2-transformed Heavy/Light ratio of quantified proteins between the original experiment and the technical replicate to evaluate instrumental error. Sixty percent of the upregulated BCR responsive proteins were identified in both runs (depicted in black). Proteins, such as ARPC5L that are depicted in grey were identified in a single run.

4.6.2. Hit validation by Western blot

In addition to technical replication, validation of proteomic data can additionally be performed by selecting certain targets from the proteomic dataset and confirming their presence using Western blot analysis. In this study Syk and Vimentin (Vim) were two predominant proteins identified within the

phosphoproteome analysis and were selected for target validation. Figure 21 shows a Western blot analysis for Syk and Vim in pTyr immunoprecipitates, from lysates of JeKo-1 cells (IP samples). The presence of these two proteins was clearly enhanced in the immunoprecipitated proteins from lysates of Jeko-1 cells that were BCR stimulated compared to lysates of untreated cells. This observation is matched by concomitant removal of Syk, Vim and PLCγ2 from lysates of activated JeKo-1 cells post immunoprecipitation (post-IP). These results demonstrate that Syk, Vim and PLCγ2 are selectively enriched in the immunoprecipitates where BCR is stimulated, and validate my observations using MS analysis. At this point I probed these gels with antibodies against ARPC5L, but was not able to observe clear bands at this size.

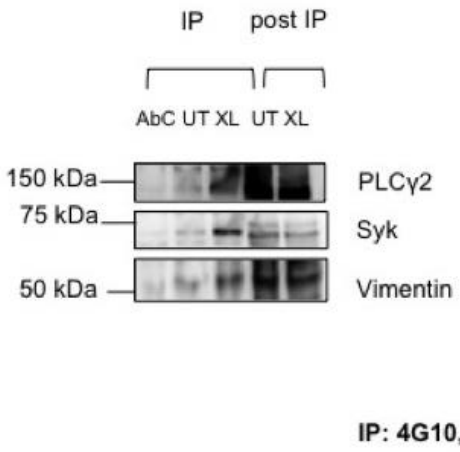


Figure 21: Syk, PLCγ and Vim are selectively enriched in BCR stimulated cells after immunoprecipitation of the pTyr co-associating network in JeKo-1 cells. Western blot analysis of the produced immunoprecipitates confirms the presence of Syk, PLCγ2 and Vim in the pTyr network, as identified by mass spectrometry.

4.6.3. Panel of cell lines

The results of the phosphoproteomic experiment suggest that the set of proteins responsive to BCR stimulation, some of which recognized to be involved in proximal signalling events, define a signalling network from this receptor. Within this network is included a protein, ARPC5L, whose function had not been defined within this context. ARPC5L and its paralog ARPC5A are part of the Arp2/3 complex important for actin reorganization. mRNA expression data for ARPC5L from the Cancer Cell Line Encyclopaedia (Figure 8), showed a link between high ARPC5L transcript levels and cell lines derived from haematological malignancies. In terms of CLL, Western blot analysis of CLL cell lysates shows varied expression levels of ARPC5L between cases (Figure 22B). Furthermore, investigation of the ARPC5L/ ARPC5A expression ratio, as has been done in previous studies, in a range of cell lines showed that B cell derived cell lines appear to have a predominance of ARPC5L expression (Figure 22A). Bearing in mind that BCR plays an important role in CLL pathophysiology, it is reasonable to speculate that varied levels of ARPC5L may also have a role to play in this disease. Considering that little is known about the function of ARPC5L, particularly in B cells, this protein was chosen for further study.

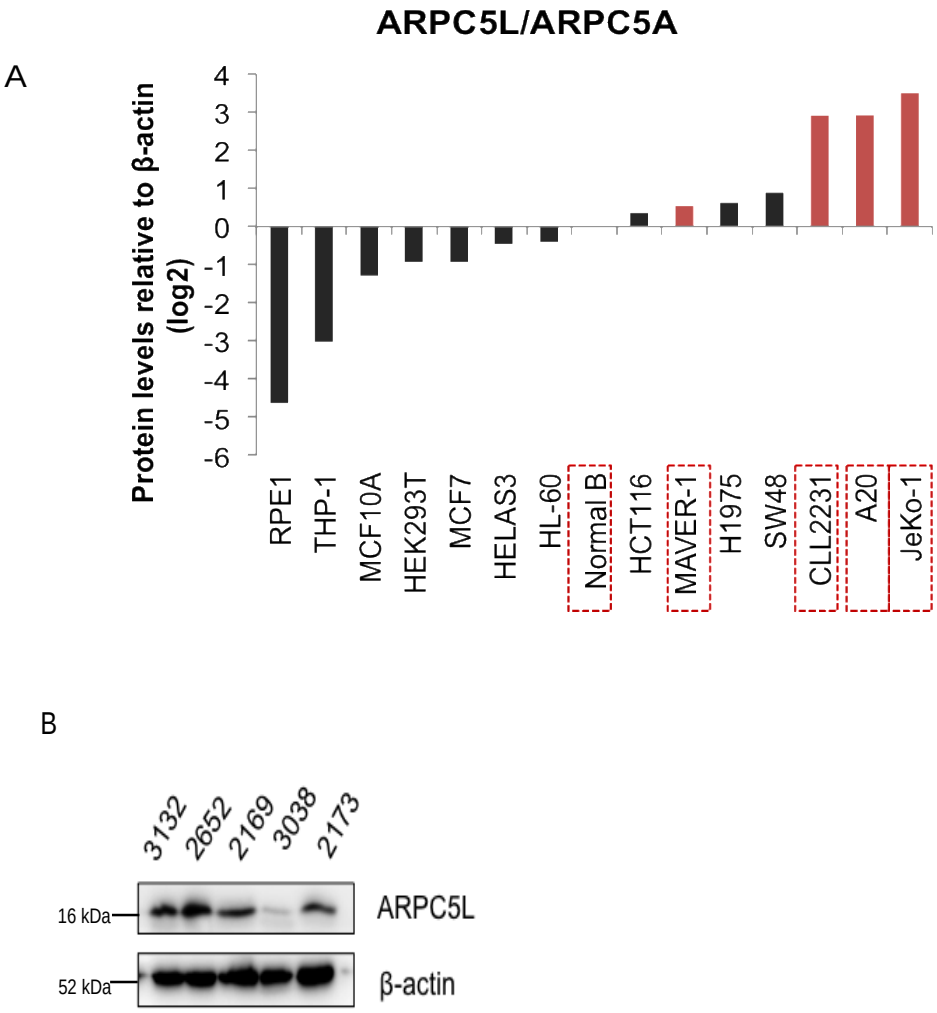


Figure 22: Quantitative analysis of ARPC5 isoform abundance in B cell lines and primary B cells: A. ARPC5L/ARPC5A ratio was quantitated by Western blotting in both malignant and non-malignant cell lines and primary cells. β – actin was used as loading control and protein levels were normalized to ARPC5L/ARPC5A ratio of normal B cells. Highlighted cell types are B-cell derived cell lines or primary B cells (n=1). B. Western blot analysis of primary CLL cells for ARPC5L levels. 10 µg of lysate were analysed by SDS PAGE and tested for ARPC5L protein expression (Abcam, Cambridge, UK). β-actin was used as a loading control (n=1).

4.6.4. Knockdown of ARPC5 paralogs in MCF7 cells

To start my investigation into the functional roles of ARPC5 paralogs, I used MCF7 cells. These cells express both paralogs, are easier to genetically manipulate compared to B cells and have well-established assays with which to study cytoskeletal phenomenon. Therefore, MCF7 cells are a good cell model to perform initial functional studies to investigate changes in behaviour after knockdown of ARPC5paralogs. Any experiments done using this model were performed after having considered the common limitations that occur when using a cell line model such as the fact that by default the heterogeneity of a disease cannot be captured as can be achieved with clinical samples, that there is limited coverage of specialised histopathological types and that the phenotypic characteristics of cultured cells change over time. In addition, looking more specifically at the suitability of MCF7 cells, these cells are a mammary epithelial cell line that does not have common genetic alterations or biomarker expression with B lymphocytes. MCF7 cells are not representative of the disease or clinically relevant for the B cell study however at this point of this project they were a powerful experimental tool allowing me to obtain initial information about the discovered protein.

Figure 23 shows that I was able to significantly reduce expression of ARPC5A and ARPC5L with the use of pooled siRNA oligonucleotides (Table 8). In addition, I noticed that when the expression of ARPC5A is reduced in response to transfection with specific siRNA, there is an increase in expression of ARPC5L compared to control levels ($p=0.0069$, Figure 23B), Conversely, when expression of ARPC5L is reduced by specific siRNA, expression of ARPC5A is observed to increase ($p=0.039$, Figure 23C). Together, these data suggest that a compensation mechanism may be operating where one ARPC5 paralogue affects expression of the other through either change in gene expression or protein stability.

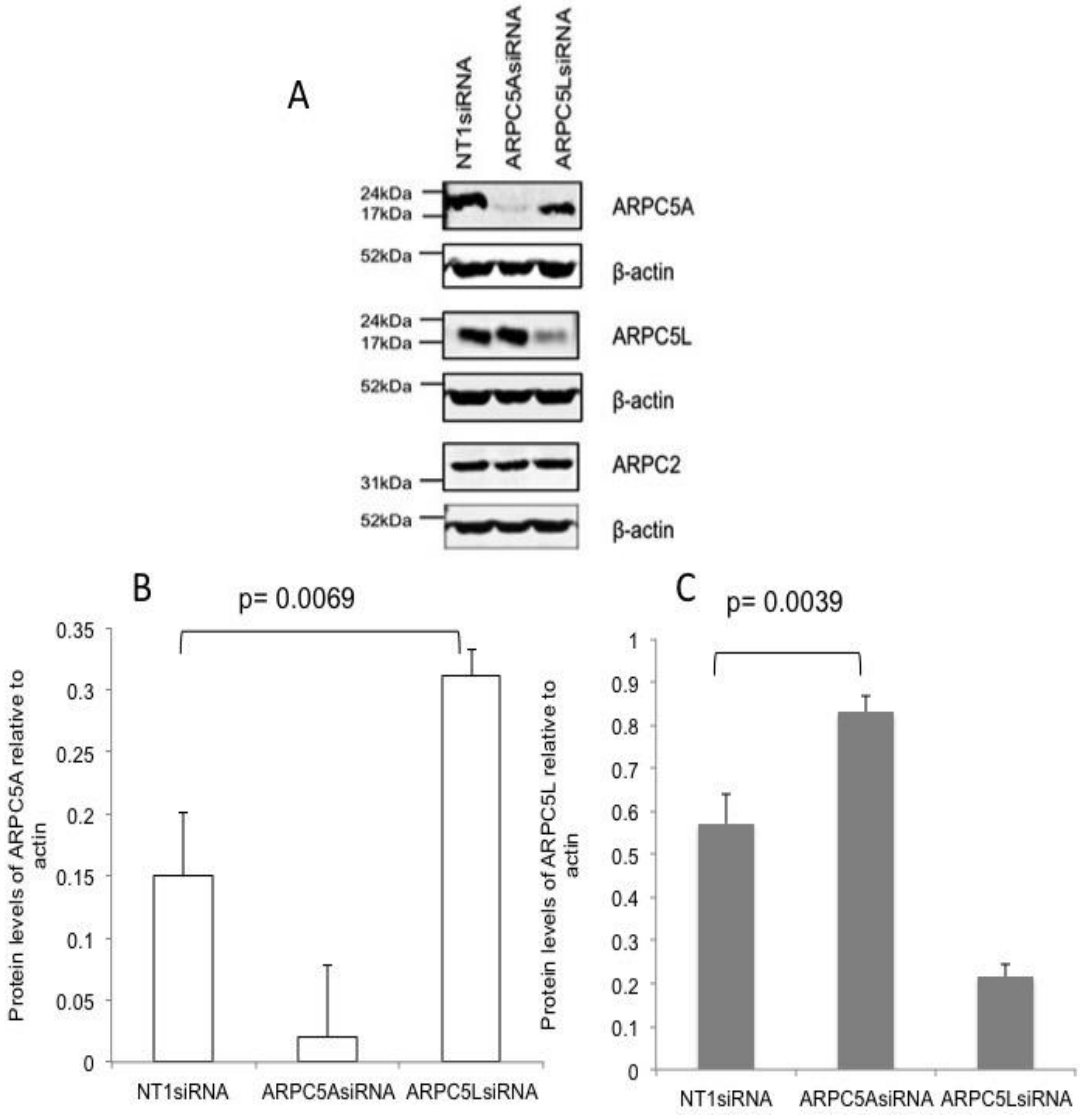


Figure 23: Knockdown of ARPC5 isoforms In MCF cells. A. Western blot analysis of indicated proteins within lysates of MCF7 cells treated with the indicated siRNAs against ARPC5A, ARPC5L and non-targeting control. 10 µg of protein within each lysate was loaded per lane. B., C. Compendium of n=3 experiments where densitometry is used to assess expression levels of ARPC5A and ARPC5L in relation to β-actin in MCF7 cells treated with siRNA to ARPC5A and ARPC5L, respectively. Error bars represent standard error of the mean. Statistical analysis was performed to look at increase of paralogue expression when expression of the other is reduced, using a student's t-test for paired data. ARPC2 was used as a negative control for potential

transfection off target effects. For this data set a nonparametric statistical test, which does not assume normality would have been more appropriate.

4.7. Discussion

In this chapter, I performed an open discovery proteomics approach in order to globally characterize active BCR signalling in JeKo-1 cells. I found that I was able to identify 854 proteins in the pTyr-associated network of BCR stimulated JeKo-1 cells, and within this set of proteins 60 were responsive to BCR stimulation. This approach was one of the first attempts to globally study B-cell receptor signalling when these experiments were performed at the beginning of the work that lead to generation of this thesis.

To verify the repeatability of the experiment I performed a replicate experiment by analysing the same sample using the same parameters and instrumentation. As shown in Figure 20 there is a considerable degree of overlap between the data derived from the original experiment and that derived from this technical replicate. This result is in keeping with those of a previous study where a 44%-46% overlap in the peptides was detected between pairs of replicate samples depending on whether the same or different mass spectrometers were used (176). In this way my data demonstrate good reproducibility between repeat measurements, and suggests that the results gained were not the result of instrumental error. Conclusions drawn from the data could be considerably strengthened by biological replication of the experiment, especially regarding ARPC5L. This protein was observed in the first proteomics run with a total of 2 ARPC5L distinct peptide sequences identified. but was absent from the technical replicate dataset. Although a full replication of the proteomics approach is not included within this thesis, a smaller scale experiment employing Western blot as a validation method was performed (Figure 21). This smaller experiment demonstrated that three of the hits identified within the proteomics approach, namely vimentin, Syk and PLCγ2, were present within the anti-pY immunoprecipitates from lysates of BCR-stimulated cells but not within those from lysates of unstimulated cells. However, this validation method could not be used with respect to verification

of ARPC5L because of similarity in MW with the Ig light chain of the anti-pY antibodies used to immunoprecipitate proteins from cell lysates in my experiments. Here I was unable to reliably discriminate between Ig light chain and ARPC5L, and no firm conclusion of validity could be drawn. Nevertheless, because there is agreement with other aspects of the BCR signalling pathway, this experiment therefore gives confidence in support of the conclusions drawn from the original proteomics approach,

According to my findings in this part of the study, three major interconnecting clusters are formed when mapping the network of BCR signalling derived from our proteomic dataset. These clusters, represented by pathways derived from STRING analysis (Figure 19), seem to mirror the processes that are necessary for B-cell activation: Binding of antigens to the BCR induces signalling cascades involving CD79, Syk, PLCγ2 and Gab1, actin reorganization is also induced and this is followed by antigen internalization for processing and presentation (177). Thus, the dataset I generated using this proteomic approach confirms the validity of this method for the analysis of BCR signalling. Furthermore, my data further suggested a distinct link between induction of phosphorylation signaling cascades and cytoskeletal reorganization. This link is supported by demonstration of the role cytoskeleton plays in translocation of the BCR into lipid rafts in order to bring it in the vicinity of Src family kinases to start the signalling process, and for BCR internalization and transport of Ags to the endosomal compartments where they are fragmented and loaded on to MHC class II proteins to be seen by cognate T cells (178).

Within the set of 60 proteins identified to be responsive to BCR signalling the prominence of the cytoskeletal proteins in my data in combination with the importance of actin-associated regulation of BCR signalling, the central motif of this study, lead me to investigate the Arp2/3 complex and its functional role in B cell malignancies. I found that a majority of Arp2/3 complex components is present within this dataset, and I decided to focus on ARPC5L and its paralog ARPC5A, understudied isoforms of the proteins involved in the Arp2/3 complex. Interestingly, the investigation of ARPC5A and ARPC5L protein levels in various malignancies shows that the latter has high levels in haemic

malignancy, a finding that agrees with that reported on the CCLE and the Immuno-Navigator databases (179). In preparation for functional studies of ARPC5L and ARPC5A in the next chapter I show that I was able to manipulate protein expression of these isoforms in MCF7 cells, an initial model cell line. MCF7 cells, a mammary epithelial cell line were used at this point, these cells were convenient to use because they are an adherent epithelial cell line that is easy to transfect with siRNA. Thus, treatment of this cell line with pooled siRNA targeting ARPC5A and ARPC5L resulted in quantitative reduction of protein expression of these paralogs. Interestingly, upregulation in expression of ARPC5A was observed when cells were treated with siRNA targeting ARPC5L and vice versa. This could be because each paralog is involved in regulating the stability of the other. This phenomenon has not been described for ARPC5 paralogs, but has been reported of other paralog pairs such as SHIP1 and SHIP2 (180).

5. Chapter – Functional investigation of ARPC5 paralogs in MCF7 and MAVER-1 cells

The discovery proteomics part of this thesis showed that ARPC5L is a component of the BCR signalling complex. ARPC5L is an understudied protein whose role in B cell biology is unknown. This chapter therefore examines the functional role of this protein, particularly with respect to cell migration and the effects of BCR crosslinking on cell migration as we outline below.

Cell migration occurs in a wide variety of biological processes extending from inflammatory response and wound healing to malignant cell metastasis (181). With respect to CLL cells, trafficking occurs between various haemic tissues to ensure access to the support they need from immune and stromal cells (182). When these malignant lymphocytes remain in the nodes, this leads to lymphadenopathy, a sign of advanced disease and poor prognosis (183). Although this process is crucial and its mechanism very important, little is known about the dynamics of tissue homing, migration, and recirculation of CLL cells out of and into this microenvironment.

At the molecular level, cell migration involves the generation of branched actin networks that power the protrusion of the plasma membrane in lamellipodia (184). The Arp2/3 complex, a highly conserved group of proteins consisting of 7 different subunits, is the molecular machine that nucleates these branched actin networks. ARPC5L is part of this complex and has a paralog, ARPC5A, with which it shares 67% homology (123). It is already known that these paralogs differentially influence the actin nucleating activities of the Arp2/3 complex, modulating the ability of cortactin to stabilize actin branching (134).

In this chapter I hypothesized that ARPC5 isoforms affect Arp2/3 complex-mediated migration and could impact on lymphocyte trafficking towards the lymph node environment. I set out to study the role of ARPC5L in B cell biology, first by investigating ARPC5A and ARPC5L function in a model system of cell migration (MCF7 cells), and then examining how these paralogs

affect B cell migration in the presence or absence of BCR signalling. The aims of this chapter are:

- To manipulate expression of ARPC5 paralogs in a B cell line.
- To test the effect of the changes in ARPC5A and L expression in functional readouts.
- To look at how ARPC5L/ARPC5A expression ratios vary in clinically stratified CLL cells.
- To test whether the ARPC5 related findings observed in the B cell line are relevant in CLL.

5.1. Materials and Methods

5.1.1. Knockdown studies by small interfering RNA (siRNA) in MAVER-1 cells

MAVER-1 cells were transfected by nucleofection. $2x10^6$ cells/transfection were washed twice with sterile pre-warmed PBS at 37°C. For each transfection the cells were resuspended in 100 µl of nucleofection solution V (Lonza Group, Switzerland) containing the siRNA or plasmid (for overexpression studies) of choice. Program X-01 was used for nucleofection using the Amaxa nucleofector (Lonza Biologics plc, UK). Directly following nucleofection the cells were transferred to 500 µl of pre-warmed RPMI media within a 1.5 ml eppendorf tube, and maintained at 37°C until all transfection procedures were complete. This was followed by transfer of the cells to more formal culture conditions (24 well plate) where they could be kept for 24 h under optimal conditions. Next day, the media was changed, and the cells were cultured for another 48 h before performing further experiments. Table 8 lists the sequences targeted by each oligonucleotide.

Target protein	Target sequence	
ARPC5A	GCAGGCAGCAUUGUCUUGA	ON-TARGETplus SMARTpool siRNA J-012080-05
ARPC5A	GUGUGGAUCUCCUAAUGAA	ON-TARGETplus SMARTpool siRNA J-012080-06
ARPC5A	GAAUAUGACGAGAACAAGU	ON-TARGETplus SMARTpool siRNA J-012080-07
ARPC5A	GCAGUUCAAUCUCUGGACA	ON-TARGETplus SMARTpool siRNA J-012080-08
ARPC5L	UCGACGAAUUUGACGAGAA	ON-TARGETplus SMARTpool siRNA J-014690-17
ARPC5L	CUUAGCAGUAGGAGGACUA	ON-TARGETplus SMARTpool siRNA J-014690-18,
ARPC5L	GCGUUGACUUGUUAAUGAA	ON-TARGETplus SMARTpool siRNA J-014690-19
ARPC5L	GAUCCAAGGGCUGUGGUAA	ON-TARGETplus SMARTpool siRNA J-014690-20
NT1	UGGUUUACAUGUCGACUAA	ON-TARGETplus Non-targeting siRNA #1 D-001810-01

Table 8: siRNA sequences for ARPC5 isoforms and controls. All siRNAs including a non-targeting control (NT1) were purchased from Dharmacon (GE Healthcare UK Limited, Buckinghamshire). siRNAs against ARPC5 and L were purchased as pools of 4 individual siRNAs (smartPOOL®).

5.1.2. Transwell migration

For this assay, 8 μm pore size inserts (Fisher Scientific, UK Ltd) were placed in transwell plates (Fisher Scientific, UK Ltd). The bottom of the wells was covered with poly-HEMA in order to avoid adherence of migrated cells. MAVER-1 cells (5×10^5 cells) were added to the inserts, and each condition was measured in triplicate. BCR was stimulated when required by adding 20 μg/ml of $F(ab')_2$ goat anti-human IgM to the cells at the beginning of the experiment. CCL21 (1 μg/ml) (R&D Systems, Abingdon, UK) or CXCL12 (100 ng/ml) (Abcam, Cambridge, UK) was then added to the bottom wells (concentrations previously shown to induce maximum transwell migration). The plates were then incubated for 6 hours under normal culture conditions. After incubation, the undersides of the inserts were scraped to remove any cells that had recently transmigrated, and these were added to cells harvested from the bottom of the wells (Figure 24). Transmigrated cells were then counted with a haemocytometer, and the difference between input and migrated cells was calculated. For each migration condition, three identical replicates should be performed.

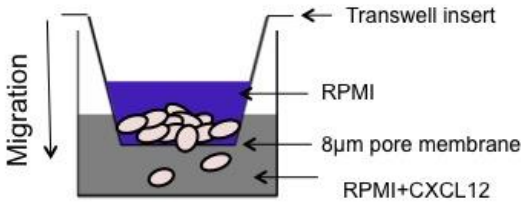


Figure 24: Transwell migration assay. For the transwell migration assay, MAVER-1 cells are placed on the upper layer of a 8 μm pore cell permeable membrane and RPMI containing the chemotactic agent is placed below the membrane. Following an incubation period of 6 h, the cells that have migrated through the membrane are stained and counted.

5.1.3. Wound healing assay

To perform wound healing or “scratch” assays MCF7 cells were plated into 6-well cell culture plates and grown in 10% FBS containing DMEM medium to confluence. The cells were washed with, serum-free medium and a scratch was made across the cell layer in the middle of the well using a p200 sterile pipette tip (Figure 25). The plate was washed once more with medium and then photographed using a live-cell imaging setup with a motorized scanning table and a stage incubator using a Nikon Ti-E eclipse microscope. The scratch was imaged using an identical aspect every 15min over a period of 48h. Movies were processed using NIS-Elements software (Nikon) and distances were calculated using ImageJ software. All experiments were performed at least three times, on three different days.

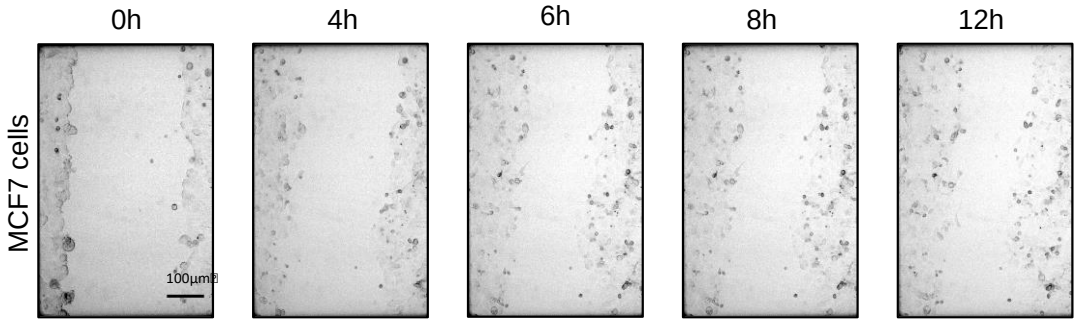


Figure 25: Wound healing assay of MCF cells. MCF7 cells were plated in 6-well plates, grown to confluency, and the formed monolayer was wounded with a pipette tip. Wound healing was documented using a Nicon Ti-E microscope during a 12-hour incubation, scale bar: 100 µm.

5.1.4. In vitro cell proliferation assay

Cell proliferation of the lentivirus-infected MCF7 clones and control cells was assessed by BrdU incorporation using a colorimetric BrdU ELISA assay kit (Roche Diagnostics, UK). At the beginning of the experiment cells were seeded at $1x10^5$/well of a 96 well plate in 100 µl of culture medium. 10µl of BrdU solution was added to each well and cells were cultured under normal conditions overnight. The plate was then centrifuged, the supernatant was removed by inversion and the plate was left to dry for 1h at 60°C. The assay was then carried out according to the manufacturer's instructions, and absorbance at 450 nm was read using a POLARstar Omega plate reader (BMG Labtech, Aylesbury, UK).

5.1.5. Lentiviral constructs/shRNA

I aimed to generate stable cell lines as tools to further study the effect of ARPC5A and L knockdown within different functional assays. To achieve this cell lines (MCF7 and MAVER1) were infected with lentivirus prepared from the MISSION® shRNA library (Sigma-Aldrich, UK) by Dr Mark Glenn. The shRNA sequences *(*the RNAi *Consortium number)* used for each isoform are listed in Table 9. This table also includes the scrambled control shRNA sequence used to prepare negative control lentivirus particles.

TRC Number	Sequence
TRCN0000 147550	CCGGGATCTGATAGTCTATGCCTTTCTCGAGAAAGGCA TAGACTATCAGATCTTTTTTG
TRCN0000 147583	CCGGGAAAGTGCTCACAAACTTCAACTCGAGTTGAAGT TTGTGAGCACTTTCTTTTTTG
TRCN0000 147584	CCGGGTCTGTTTCCTAAATCCTGTTCTCGAGAACAGGA TTTAGGAAACAGACTTTTTTG
TRCN0000 150194	CCGGGCGTTGACTTGTTAATGAAGTCTCGAGACTTCAT TAACAAGTCAACGCTTTTTTG
Scrambled control	CCGGCAACAAGATGAAGAGCACCAACTC-GAGTTGGTGCTCTTCATCTTGTTGTTTTT

Table 9: Sequences for shRNA clones against ARPC5A and ARPC5L and control sequences from the MISSION® shRNA library.

5.1.6. Plasmid DNA isolation and Transformation

The pLVXW-GFP-hARPC5A and pLVXW-GFP-hARPC5L plasmids used in this study were a kind gift of Professor Michael Way. 100 ng of the DNA plasmid was used to transform DH5 cells. Cells were thawed on ice, and then 50 µl were transferred into a pre- chilled tube containing the plasmids. Following gentle shaking, the tubes were placed on ice for 30 min. This was followed by heat shocking the bacteria by placing them in a water bath at 42°C for 45 sec. At this point, the tubes were incubated on ice for 2 min, and then 200 □l of Super optimal broth with catabolite repression (SOC) medium (Sigma Aldrich, UK) was added and the tubes. The tubes were placed in an incubator shaker at 37°C for 1 h at 245 RPM. 50 and 100 µl aliquots of this bacterial culture were spread on to pre-warmed Luria agar (LB) plates

containing 100 µg/ml ampicillin. The plates were then incubated for overnight at 37°C. The following a single colony was picked and a 5 ml culture of LB medium containing 100 µg/ml ampicillin was inoculated. The culture was further incubated with a loosened cap for 12-16 h at 37°C with 225 RPM constant agitation. 5 ml of the culture was added to a cryovial along with 1.5 ml of 50% sterile glycerol in order to create a glycerol stock.

5.1.7. Plasmid DNA digestion and validation

To verify the identity of the plasmids used in this study, single and double digestions using specific restriction enzymes were performed. 500 ng of plasmid was mixed with 1 µl of NotI for single digestion to linearize the plasmid or with 0.4 µl EcoRI and 0.4 µl BamH1 for double digestion of the plasmid. 4 µL of digestion CutSmart® Buffer was added, and the total digestion reaction volume was topped up to 20 µl with nuclease-free water. The digestion took place for 1 h at 37°C, and then the DNA fragments separated by electrophoresis using a 0.8% agarose gel. The sizes of the produced bands allowed us to confirm the plasmid map in Figure 26. All restriction enzymes and buffers used were from New England Biobs, Ipswich, UK.

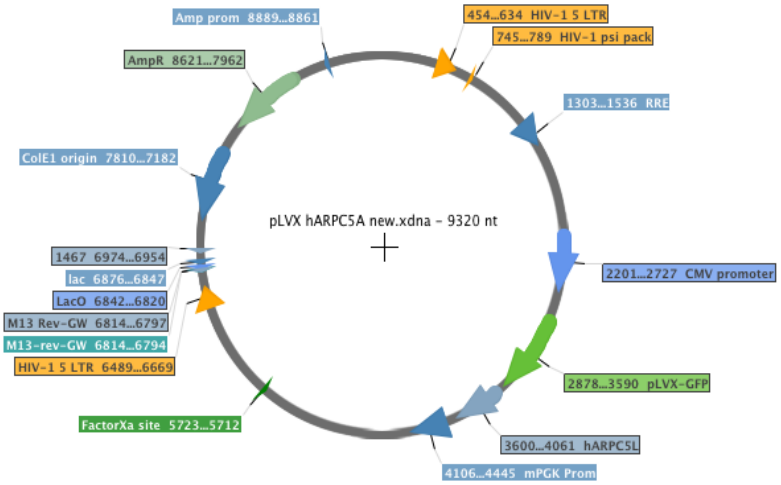


Figure 26: Validation of pLVX-GFP-hARPC5L plasmid. A. Plasmid map for pLVXW-GFP-hARPC5A generated with Serial Cloner 2.6 shows the ARPC5L insert in the pLVXW vector. B. The pLVXW-GFP-hARPC5A plasmid was digested using the NotI, EcoRI, BamH1 restriction enzymes for validation purposes.

5.1.8. Plasmid DNA and maxi-preparation (Maxiprep)

For purification of plasmid DNA, 150 ml of LB broth with 100 µg/ml ampicillin was inoculated with 150 µl of the transformed DH5 bacterial cultures from above. Following culture for 24 h, DNA plasmids were isolated and purified using a QIAGEN Plasmid Maxi Kit (QIAGEN, Manchester, UK) according to manufacturer's instructions. Purity and quantity of the resulting DNA was checked using Nanodrop 2000 spectrophotometry.

5.1.9. Overexpression

The pLVXW-GFP-hARPC5 and pLVXW-GFP-hARPC5L expression constructs or the control pmaxGFP vector (Lonza, Cambridge, UK) were

transfected into the MAVER-1 cell line using nucleofection as described in 5.1.1. The amount of plasmid DNA that was used for transfection was optimized using flow cytometry and I observed that transfecting the MAVER-1 cells with 4µg of plasmid resulted in 14% transfection efficiency for pLVXW-GFP-hARPC5A and 12% for pLVXW-GFP-hARPC5L. Under these conditions cell viability was maintained at >80%.

5.1.10. Deconvolution of siRNA smartPOOL against ARPC5A

The use of pooled siRNA oligonucleotides was used in this study to promote competition between different siRNAs for optimal silencing and minimizing of off-target effects associated with individual siRNAs. For the purposes of deconvolution, the set of four different siRNAs targeting each ARPC5 isoform were individually evaluated, each used at 10 nM, and compared with MAVER-1 cells transfected with negative control siRNA (40 nM) as well with the siRNA pool (40nm) (Table 8). The level of knockdown for each oligonucleotide was analysed by Western blotting.

5.1.11. Studies with primary CLL cells

Primary CLL cells were provided by Dr David Allsup (University of Hull), these cells were collected from patients with informed consent and used in accordance to ethical agreements in place at the Universities of Hull and Liverpool (Liverpool Research Ethics Committee #16/NW/0810 reviewed at Liverpool East Research Ethics Committee and the Hull and East Yorkshire Ethics Committee #08/H1304/35, renewed to 2023). Each sample was used for a defined experiment and its use was recorded. The phenotypic features of CLL cells from the selected patients is presented in Tables 10 and 11 (Appendix).

Sample ref	Lymphadenopathy Neck	Lymphadenopathy Axillae	Lymphadenopathy Groin	Splenomegaly	Binet Stage	VH status
16	FALSE	FALSE	FALSE	FALSE	A	UM
70	FALSE	FALSE	FALSE	FALSE	A	M
116	FALSE	FALSE	FALSE	FALSE	A	M
145	FALSE	FALSE	FALSE	FALSE	A	M
151	FALSE	FALSE	FALSE	FALSE	A	M
176	FALSE	FALSE	FALSE	FALSE	A	M
178	FALSE	FALSE	FALSE	FALSE	A	UM
205	FALSE	FALSE	FALSE	FALSE	A	-
248	FALSE	FALSE	FALSE	FALSE	A	M
88	FALSE	TRUE	TRUE	TRUE	B	M
91	TRUE	TRUE	TRUE	TRUE	B	M
93	TRUE	TRUE	TRUE	TRUE	C	UM
99	TRUE	TRUE	TRUE	FALSE	C	UM
171	FALSE	TRUE	TRUE	TRUE	C	UM
139	TRUE	TRUE	TRUE	TRUE	C	UM
117	TRUE	TRUE	FALSE	FALSE	B	M
55	FALSE	FALSE	TRUE	TRUE	C	M

Table 10: Primary CLL cells from the University of Hull patient database, characterized for a variety of parameters describing the clinical course of the disease.

5.1.12. CXCR4 Surface Expression Analysis in the presence of BCR crosslinking

MAVER-1 cells in RPMI media were crosslinked with 20 µg/ml F(ab')$_2$ goat anti-human IgM and cultured for 6 hours. As described in Chapter 3.2.1, cells were washed once in staining buffer (PBS, 0.5% BSA, 0.05% azide) and incubated in the presence of CXCR4 antibodies for 1 h. After two washes,

primary antibodies were detected using a FITC-conjugated F(ab')$_2$ fragment of goat anti–mouse IgG. Signals were acquired using an Attune™ flow cytometer (Life Technologies Ltd, Paisley UK).

5.1.13. Spreading assays

12 mm glass coverslips were coated with 40 µg/ml whole goat anti-mouse IgM (Jackson ImmunoResearch Europe Ltd, Suffolk, UK) overnight at 4°C. MAVER-1 cells were incubated on the coverslips at 37°C for predetermined times, and then fixed with 4% paraformaldehyde for 20 minutes at room temperature. The cells were then permeabilized with 0.5% Triton X-100. The samples were blocked with PBS containing 3% goat serum for 30 minutes at RT, then incubated with Alexa Fluor 594 phalloidin (1:40 in PBS+3% BSA) for 20 minutes at RT. Following staining the samples were rinsed three times in PBS, mounted on to a coverslip using Mowiol anti-fade reagent (Fisher Scientific UK Ltd, Loughborough,UK). Immunofluorescence images were taken using a Nikon Eclipse Ti-E microscope with a digital camera (CoolSNAP EZ Turbo 1394; Photometrics). The images were then processed using NIS-Elements Software (Nikon). The spreading area of MCF7 cells were quantified using ImageJ, by selecting 10 cells in each frame at time 0 and 15 minutes.

5.2. Results

5.2.1. Knockdown of ARPC5 paralogs impacts MCF7 cell migration in an assay of wound healing.

I began investigating the functional role of the ARPC5A and ARPC5L paralogues with wound-healing assays because they are simple, inexpensive and effective for studying directional cell migration *in vitro*. This method models cell migration during wound healing *in vivo*. The basic steps involve allowing

the cells to attach, spread, and form a confluent monolayer. This is followed by the creation of a “wound” in the cell monolayer, and the cells imaged at 15-minute intervals during wound closure.

Initial siRNA knockdown experiments targeted ARPC5 and ARPC5L separately in the MCF7 cells (Figure 27A). In addition, I also attempted simultaneous knockdown of the ARPC5 paralogues to examine if it was possible to significantly reduce both of their expression (Figure 27A).

Figure 27B shows that control MCF7 cells (NT1) close the wound by 24.9% following 12 h of culture. Knockdown of ARPC5A significantly increases the rate of wound closure to approximately 65% ($p=0.0129$). In contrast, ARPC5L knockdown does not impact on the rate of wound closure compared to control despite clear reduction in ARPC5L protein expression (Figure 27B). These results suggest that ARPC5A knockdown increases the ability of MCF7 cells to migrate.

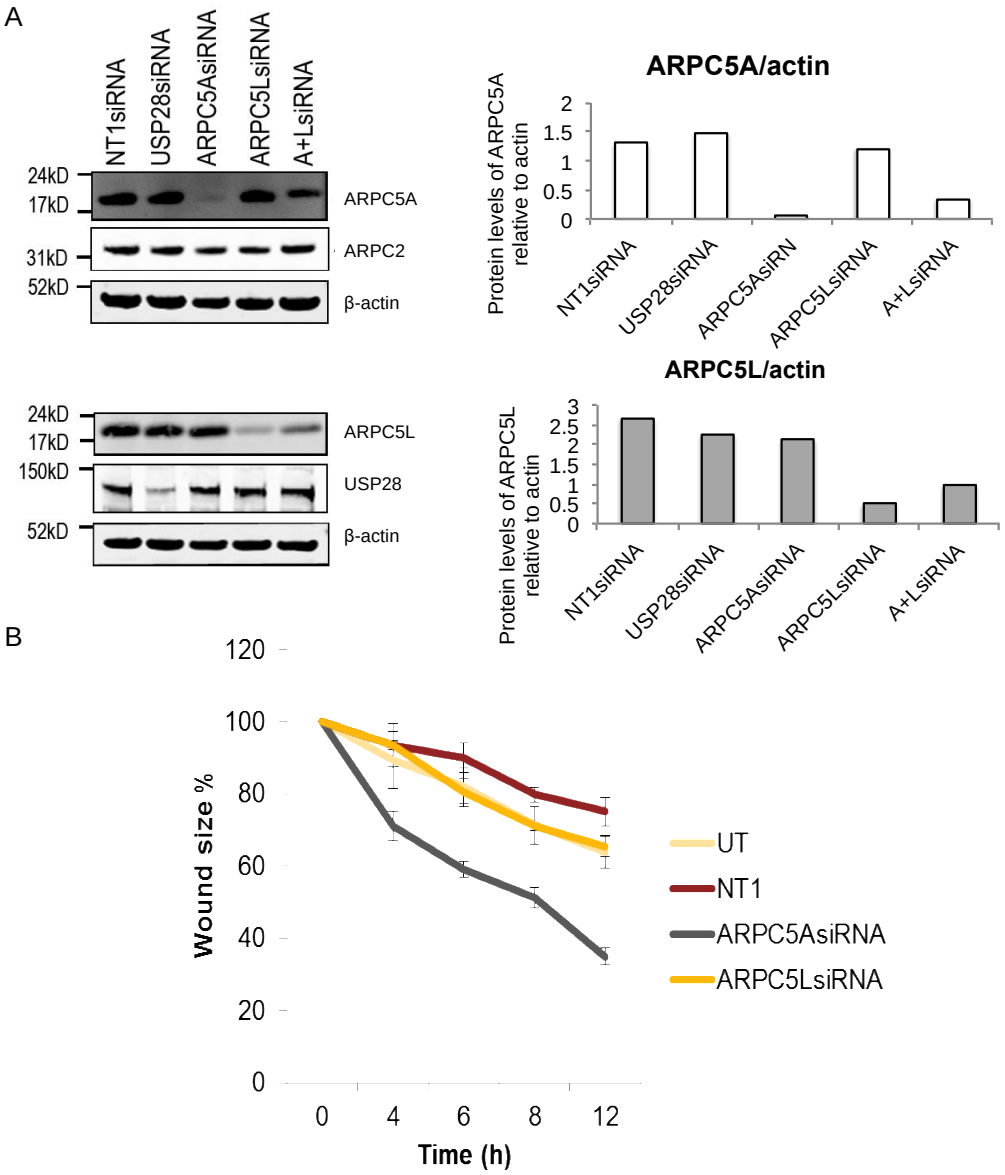


Figure 27: ARPC5A knockdown in MCF7 cells increases migration in wound healing assay. A Western blot analysis of ARPC5A and L within lysates of MCF7 cells treated with the indicated siRNAs. For the ARPC5A+ARPC5L simultaneous transfection, the siRNA concentration of each paralogue was halved. USP28 was used as positive control for transfection efficiency. ARPC2 and actin were used as a loading controls. B. Compendium of n=3 experiments using siRNA to ARPC5A and ARPC5L, respectively. Following siRNA knockdown of ARPC5 isoforms, MCF7 cells were grown to 90% confluence, a single wound was made in the centre of cell monolayer and

cell debris was removed. After 12 h of incubation, the wound closure areas were visualized at indicated timepoints and the length of wound areas were measured using ImageJ. Error bars represent standard error of the mean of three independent experiments. Statistical analysis was performed using a student's t-test for paired data, the p value for wound healing of ARPC5A knockdown MCF7 cells compared to control is 0.001. For this data set a nonparametric statistical test, which does not assume normality would have been more appropriate.

5.2.2. Single cell migration of MCF cells is affected by knockdown of ARPC5 paralogs

To validate the wound healing assay, I examined migration at single-cell level. I did this in two ways; firstly, by examining sparsely seeded cells and secondly, by examining MCF7 cells that were located at the middle of the wound in the above assay. Sparsely seeded cells typically did not move over long distances (185) making this assay difficult to fully interpret using the Chemotaxis and Migration software (Ibidi) available to me. Nevertheless, knockdown of ARPC5A appeared to increase cell movement whereas knockdown of ARPC5L had no effect. Tracked single cells within the wound healing assay moved greater distances that were easy to measure reproducibly. Figure 28 shows that single cells transfected with siRNA against ARPC5A to lower expression of this protein (Figure 28A, B) travel significantly longer distances than cells transfected with control siRNA ($p=0.0012$). Importantly, the directionality of the cells does not seem to be affected by the knockdown of either isoform.

Taken together with the results from the wound healing assay, these data suggest a role for ARPC5 paralogue expression in cell movement.

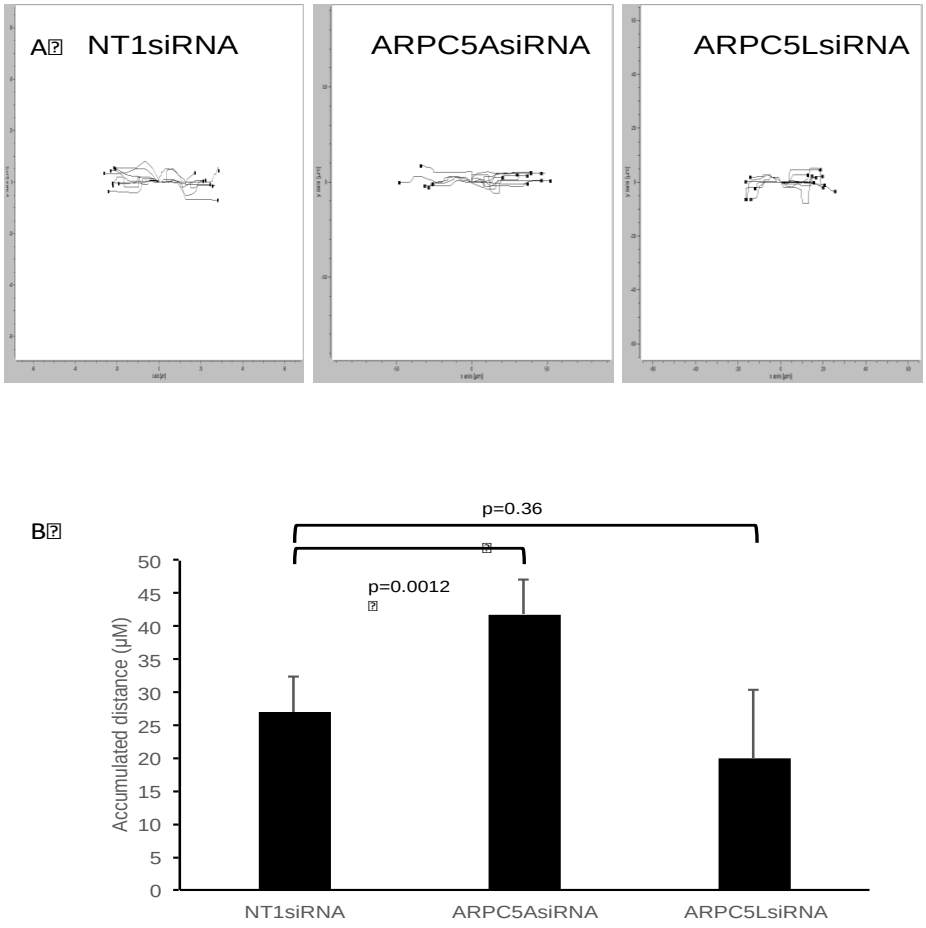


Figure 28: ARPC5A knockdown in MCF7 cells increases single cell migration. A. Cell trajectory plots of individual MCF cells tracked in the wound healing assay over 12 hours were analysed using ImageJ software in combination with Manual Tracking and Chemotaxis Tool plug-in (ibidi), demonstrating both directionality and Euclidean distance. In each case, 15 representative cells were tracked across a sequential series of 48 images (12 hours). B. Quantitation of cell migration distance in three independent experiments by the Manual Tracking and Chemotaxis Tool (ibidi). Error bars refer to standard error of the mean. The statistical significance of the difference in migration between knockdown ARPC5A or ARPC5L MCF7 cells and control was calculated using a paired student's t-test (p=0.0012). For this data set a nonparametric statistical test, which does not assume normality would have been more appropriate.

5.2.3. Ectopic expression of ARPC5 paralogs and effect on MCF7 cells.

To validate my observations on the relationship of ARPC5 isoforms and migration I used pLVXW-GFP-ARPC5A pLVXW-GFP-ARPC5L plasmids (a gift from Professor Michael Way) to ectopically express human ARPC5A/L isoforms in MCF7 cells (Figure 29B)

Analysis of cell migration using the Manual Tracking plugin and Chemotaxis tool for ImageJ showed that cells overexpressing ARPC5L exhibit increased migration compared to control cells and to cells overexpressing ARPC5A. ARPC5L transfected cells travel a significantly longer trajectory (accumulated distance) and cover the Euclidean distance (the shortest linear distance from the starting point to the end point with increased velocity (Figure 29A, 29C).

Taken together, these data complement and validate our previous observations of MCF7 cell migration using siRNA to manipulate expression of ARPC5 isoforms. Thus, it appears the ratio of ARPC5A to L expression is important in terms of cell migration. High levels of ARPC5L to A facilitate migration, whereas high levels of ARPC5A to L do not affect or may even impede migration.

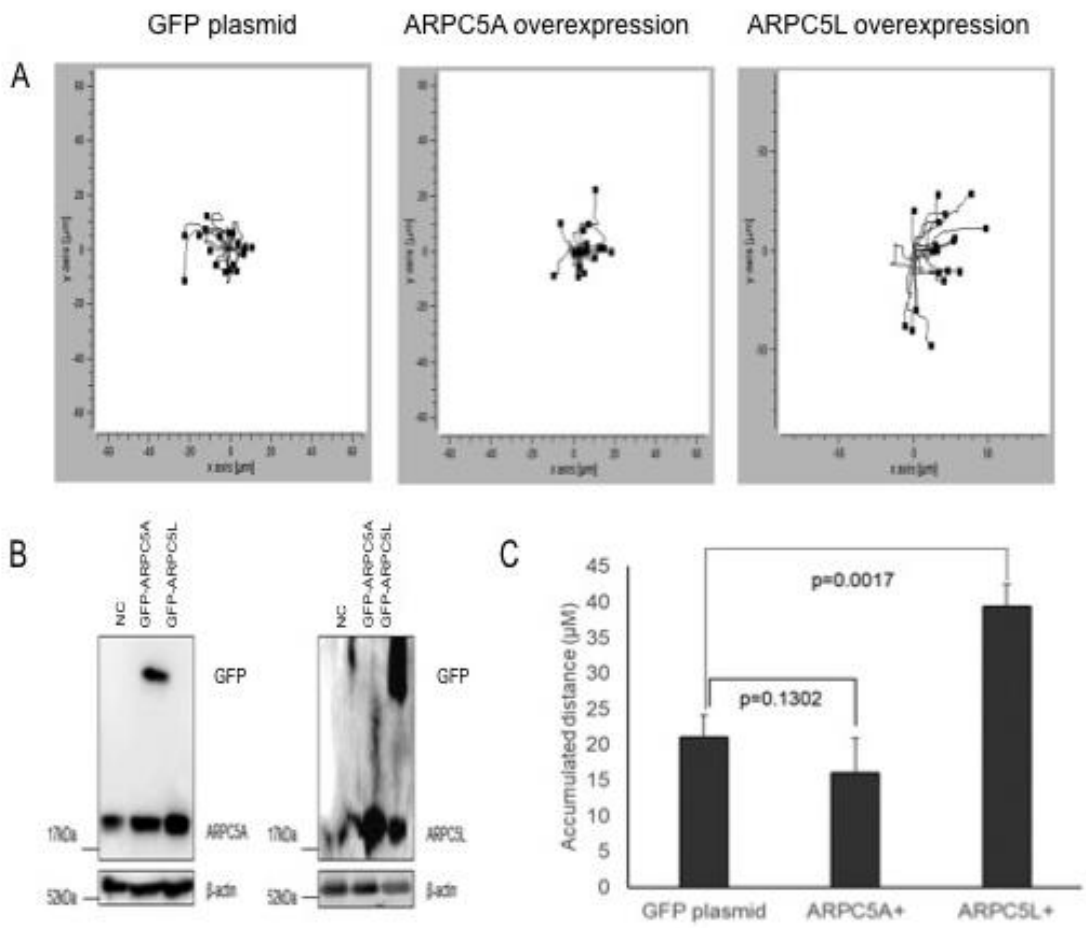


Figure 29: ARPC5L overexpression induces higher migratory capacity in MCF7 cells. MCF7 cells, transduced with pLVXW-GFP-ARPC5A, pLVXW-GFP-ARPC5L plasmids were used in a single cell migration assay where their migratory capacity was evaluated using the Chemotaxis and Migration ImageJ plugin. A. Plots of the paths of MCF7 cells overexpressing ARPC5A and L. B. Western blot analysis of MCF7 cells nucleofected with 4μg of plasmids expressing GFP-ARPC5A, GFP-ARPC5L proteins C. Graphic representation of accumulated distance travelled by the cells within 12 hours, statistical significance was calculated using a one-tailed student's *t*-test, the error bars refer to standard error of the mean of three independent experiments. For this data set a nonparametric statistical test, which does not assume normality would have been more appropriate.

5.2.4. ARPC5 paralog knockdown impacts on B cell chemotaxis and migration rate in transwell system

According to the findings of Chapters 5.2.1 and 5.2.2, knockdown of each ARPC5 isoform differentially affects cell migration of MCF7 cells. Due to this observation, I set out to look at this phenomenon in B cells using a transwell migration assay. For the B cell line assays in this chapter, the MAVER-1 cell line was used due to problems with the growth of Jeko-1 cells. For characterisation of MAVER-1 cells please see Figure 40 in the Appendix.

To induce cell migration I used CXCL12 (SDF-1), which induced significant migration of untreated MAVER-1 cells (Figure 31B). Knockdown of the ARPC5 paralogs (Figure 30A) did not seem to have any effect on spontaneous migration of the cells. However, knockdown of ARPC5A resulted in increased migration of MAVER-1 cells to CXCL12 ($p=0.000965$), whereas knockdown of ARPC5L did not have any significant effect compared to the siRNA control ($p=0.0916$). These observations agree with my results using MCF7 cells, showing that knockdown of ARPC5A increases cellular mobility.

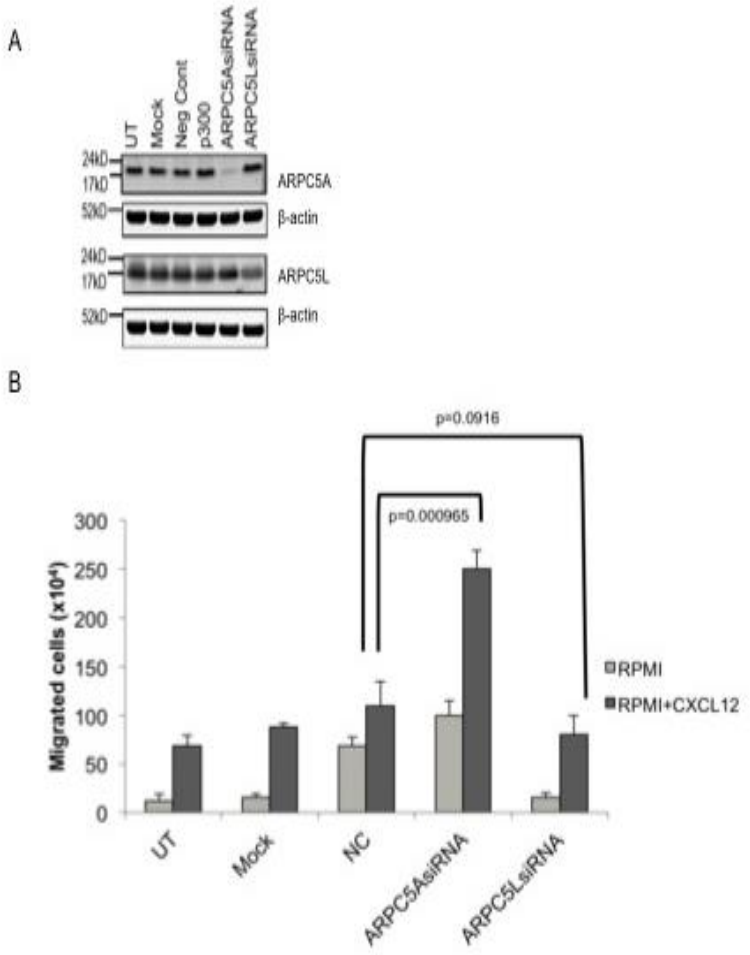


Figure 30: ARPC5A knockdown in MAVER-1 cells increases transmigration and chemotactic response to CXCL12. A. MAVER-1 cells ($2x10^6$) were nucleofected with either 40 nm of siRNA against indicated proteins or non-targeting siRNA and siRNA against p300 as negative control for transfection. B. Following culture for 12 h, the MAVER-1 cells ($5×10^5$) were added to the upper chambers of transwell plates (8 µm pore). The lower chambers of the transwell plates either contained RPMI or RPMI+CXCL12 (SDF-1) (100 ng/ml), and the assay was allowed to incubate for 6 h at 37 °C. After incubation, the transmigrated cells were harvested, washed, stained with trypan blue and counted. The error bars refer to standard error of the mean of three independent experiments. Statistical significance was calculated using a student's t-test for paired data. For this data set a nonparametric statistical test, which does not assume normality would have been more appropriate.

5.2.5. Study of the effects of ARPC5 paralog knockdown on the chemotaxis and migration rate of BCR stimulated cells

BCR crosslinking is reported to arrest B cell migration to chemokines (186). Due to the importance of BCR stimulation in our study, it was necessary to assess the impact of BCR crosslinking on the chemotactic response of MAVER-1 cells to chemokines. Figure 31A shows that MAVER-1 cell migration to CXCL12 and CCL21, chemokines that regulate lymphocyte trafficking (187), is arrested when BCR is crosslinked.

I next used siRNA to knockdown expression of ARPC5A and L and performed the transwell assay again. Figure 31B shows that knockdown of ARPC5A enhanced both spontaneous and CXCL12-induced migration of MAVER-1 cells (as is also observed in 5.2.4), and that BCR crosslinking reduced this migration in a similar way as what was observed in control transfected cells. In contrast, when ARPC5L was knocked down migration of MAVER-1 cells towards CXCL12 was not induced (lane 11), as previously demonstrated in Figure 30. This inconsistency did not allow me to investigate the possible link between the knockdown of ARPC5L and migration towards CXCL12 when the BCR is stimulated. However, this observation raises the possibility that knockdown of ARPC5L blocks chemokine induced migration, this observation could be further investigated in future studies.

In Figure 31B, migratory capacity of BCR stimulated vs non BCR stimulated, CXCL12 treated cells was compared: For control cells (NC siRNA) and ARPC5A knockdown cells BCR stimulation resulted in decreased migration (p values were 0.002 and 0.019 respectively). For ARPC5L knockdown cells, BCR stimulation appeared to increase migration (p=0.036). The data was collected from three independent experiments, for statistical analysis a nonparametric statistical test, which does not assume normality would have been more appropriate.

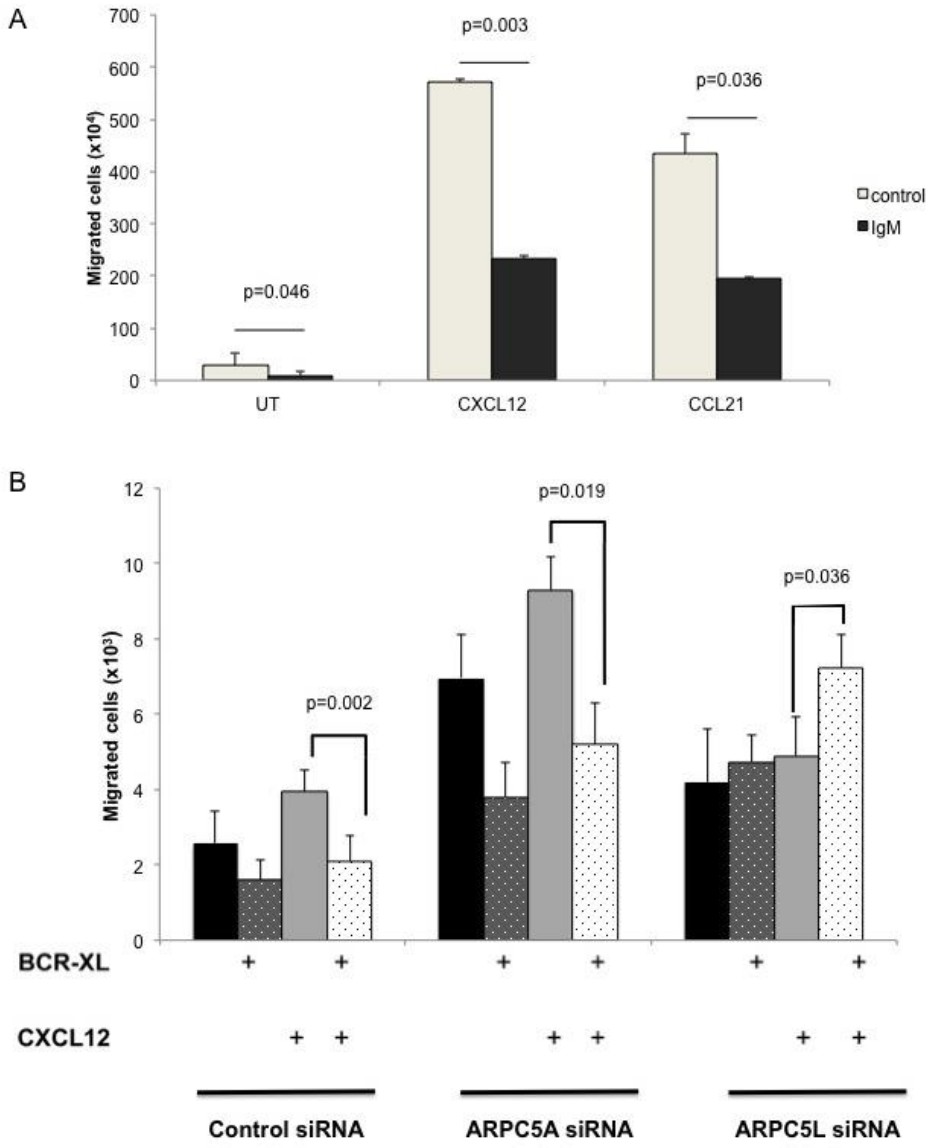
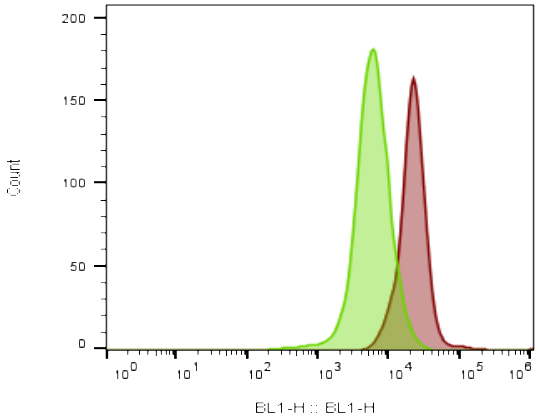


Figure 31: A. Effect of BCR stimulation on chemokinesis of MAVER-1 cells +/- knockdown of ARPC5 paralogues. A. BCR crosslinking reduces migration of MAVER-1 to chemokine. MAVER-1 cells (6×10^6) were treated with 20 µg/ml of $F(ab')_2$ goat anti-human IgM. The cells were added to the inserts of transwell plates (8 µm pore) and were incubated for 6 h at 37 °C to migrate towards a lower chamber containing RPMI, RPMI+CXCL12 (100ng/ml), RPMI+CCL21 (1mg/ml). After incubation, the transmigrated cells were washed, stained with trypan blue and counted. B. For the same assay (A), MAVER-1 cells were pretreated with siRNA against ARPC5A and ARPC5L. BCR crosslinking reduced migration of ARPC5A knockdown cells in a similar way as was

observed in control transfected cells. In contrast, knockdown of ARPC5L in MAVER-1 cells increased migration after BCR crosslinking. In (A) and (B) error bars refer to standard error of the mean of three independent knockdown and migration experiments. Statistical significance was calculated using a student's *t*-test for paired data. For this data set a nonparametric statistical test, which does not assume normality would have been more appropriate.

5.2.6. Effect of BCR crosslinking on CXCR4 levels in MAVER-1 cells

To ensure that migration arrest in BCR crosslinked MAVER-1 cells was not due to downregulation of chemokine receptor (Chapter 5.2.5), I investigated the expression of CXCR4 in unstimulated and BCR crosslinked MAVER-1 cells for six hours (the course of the chemokinesis experiment). Figure 32 shows that BCR crosslinking did not diminish CXCR4 expression on MAVER-1 cells demonstrating that migration arrest is not explained by reduction of this receptor by BCR crosslinking.



	Sample name
	CXCR4
	CXCR4_BCRXL

Figure 32: Effect of BCR crosslinking on CXCR4 levels in MAVER-1 cells. Anti-CXCR4 staining of 2x10^6 MAVER-1 cells after 6 h of incubation in medium alone or medium supplemented with F(ab′)2 goat anti-human IgM.

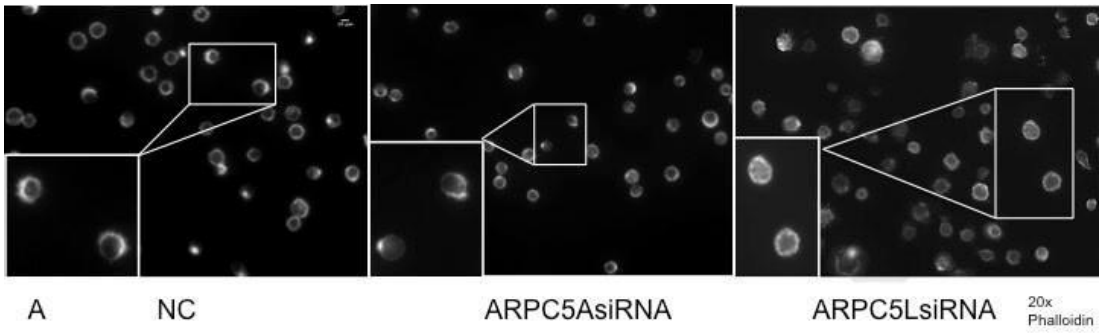
5.2.7. Analysis of effect of ARPC5A and L knockdown on BCR mediated spreading of MAVER-1 cells.

To further investigate the role of ARPC5A and L within the mechanism controlling BCR arrest of chemokine induced migration of MAVER-1 cells, I investigated how knockdown of these paralogues affected BCR induced cell spreading. The role of ARPC5A and L was investigated by looking at the ability of MAVER-1 cells to spread on anti-IgM-coated coverslips following knockdown of these paralogues with siRNA.

MAVER-1 cells were transfected with ARPC5A and L siRNA and, following 72 hours culture, were replated on coverslips precoated with anti-IgM. Cells were imaged over a period of 1 h, with half-maximal spreading being observed at 15 min. This 15 min time point was used for quantitative comparison. Figure 34A shows that cytoskeletal organization remained intact and polarization was

clearly visible in both control and ARPC5A knockdown cells. In contrast, following knockdown of ARPC5L there was a notable disruption in the ability of BCR crosslinking to polarize cytoskeleton (Figure 33A). However, in terms of cell area, knockdown of the ARPC5 paralogs did not result in a significant change in BCR-induced spreading of MAVER-1 cells in comparison to control siRNA transfected cells (p=0.078, p=0.111) (Figure 33B).

Taken together with our migration experiments, these results suggest a differential role for ARPC5A and ARPC5L in cellular events that result in cytoskeletal reorganization. Low levels of ARPC5A facilitate cell migration, but do not affect polarization. In contrast, ARPC5L seems to have an alternative role: Low levels of this paralogue do not seem to affect BCR induced cell spreading but could impact ability to polarize actin and chemokinesis.



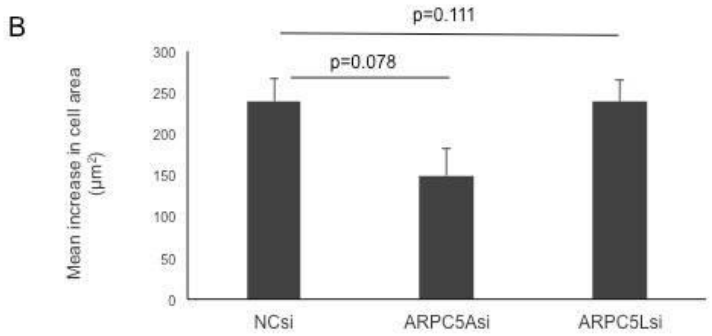


Figure 33: Decreased ARPC5A and L expression does not significantly impact BCR-induced spreading. A. MAVER-1 cells were plated onto 12 mm glass coverslips pre-coated with 40 µg/ml goat anti-mouse IgM. The cells were incubated on the coverslips at 37°C fixed at 2, 15, 30, 60 min and stained with phalloidin (scale bar 100µm). The contact area between the cell and coverslip

of spread cells at 15 min was quantified using ImageJ, by selecting 10 cells in each frame (B). Mean increase in cell area of MAVER-1 cells (µm2), error bars refer to two independent experiments. Statistical analysis was performed, using a student's t-test, for this data set a nonparametric statistical test, which does not assume normality would have been more appropriate.

5.2.8. Deconvolution

To assess potential off-target effects and validate our functional results obtained by used of the siRNA pools, I deconvoluted the oligonucleotide pools to test that they include at least one inhibitory siRNA sequence, for each ARPC5 paralog. In these experiments each siRNA oligonucleotide within the pool was used singly at a concentration of 40 nM to assess their individual effect on knockdown of the target protein. For ARPC5A all four oligonucleotides seem to supress expression of target proteIn. Interestingly, the results in Figure 34 show that knockdown of ARPC5A with the siRNA pool and clones 6,7,8 cause an increase in ARPC5L levels.

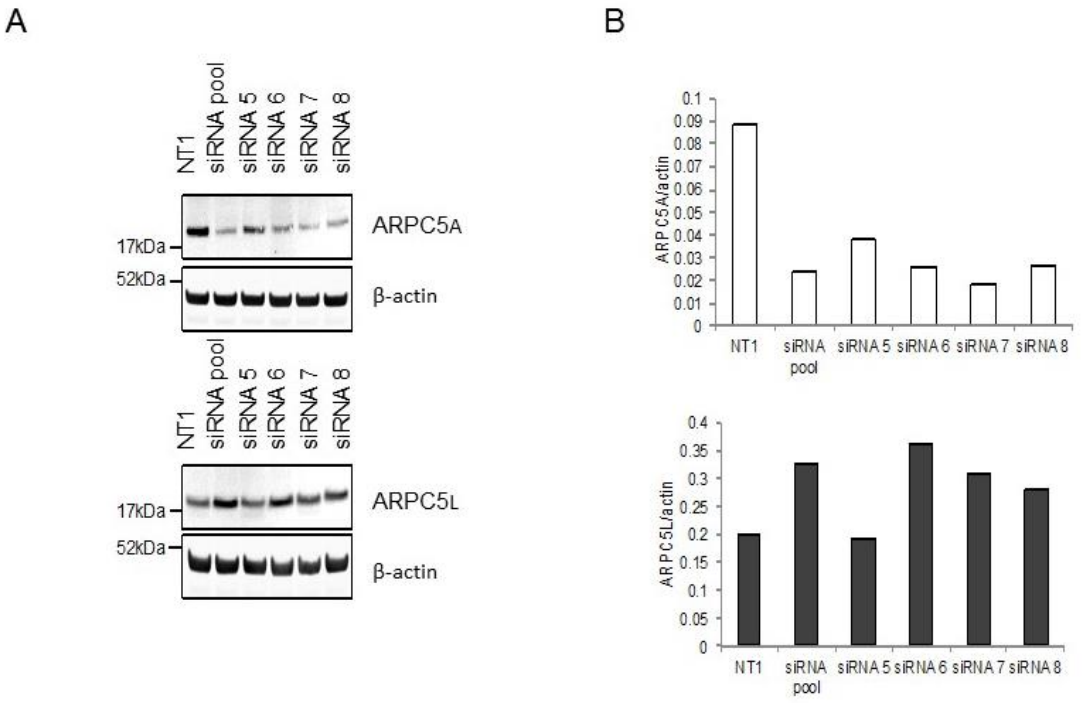


Figure 34: Western blot detection of ARPC5 paralogues in MAVER-1 cells after treatment with individual siRNA oligonucleatides and siRNA pools against ARPC5A. A. Western blot analysis of lysates derived from $2x10^6$ MAVER-1 cells, transfected with 40 nm of control, pooled, and individual siRNAS targeting ARPC5A. B. Quantitation of protein levels of ARPC5A and ARPC5 levels from (A) with β-actin used as a loading control (n=1).

5.2.9. Use of lentivirus for stable knockdown of ARPC5A and L in MCF7 cells

Our initial functional experiments, which were performed using siRNA, lead to a number of observations which, when taken together, show that the different paralogues of ARPC5 alter cellular functions linked to migration.

To expand on these observations, I used inducible shRNA and lentivirus technology to generate MCF7 cell lines with reduced expression of ARPC5A and L. For each paralogue five different shRNA clones as well as a GFP control and scrambled shRNA sequence (as a negative control) were used. Following puromycin selection the levels of knockdown were tested by Western blot. The degree of knockdown achieved ranged from 9%–52% for ARPC5A, and from 43%-82% for ARPC5L. Treatment of cells to express GFP or the scrambled (Scr) shRNA control did not seem to affect the expression of either ARPC5A or ARPC5 (Figure 35).

The generated cell lines, which stably express reduced amounts of ARPC5A and L were used in studies of morphology and cell growth to further highlight the differences between the two isoforms in MCF7 cells.

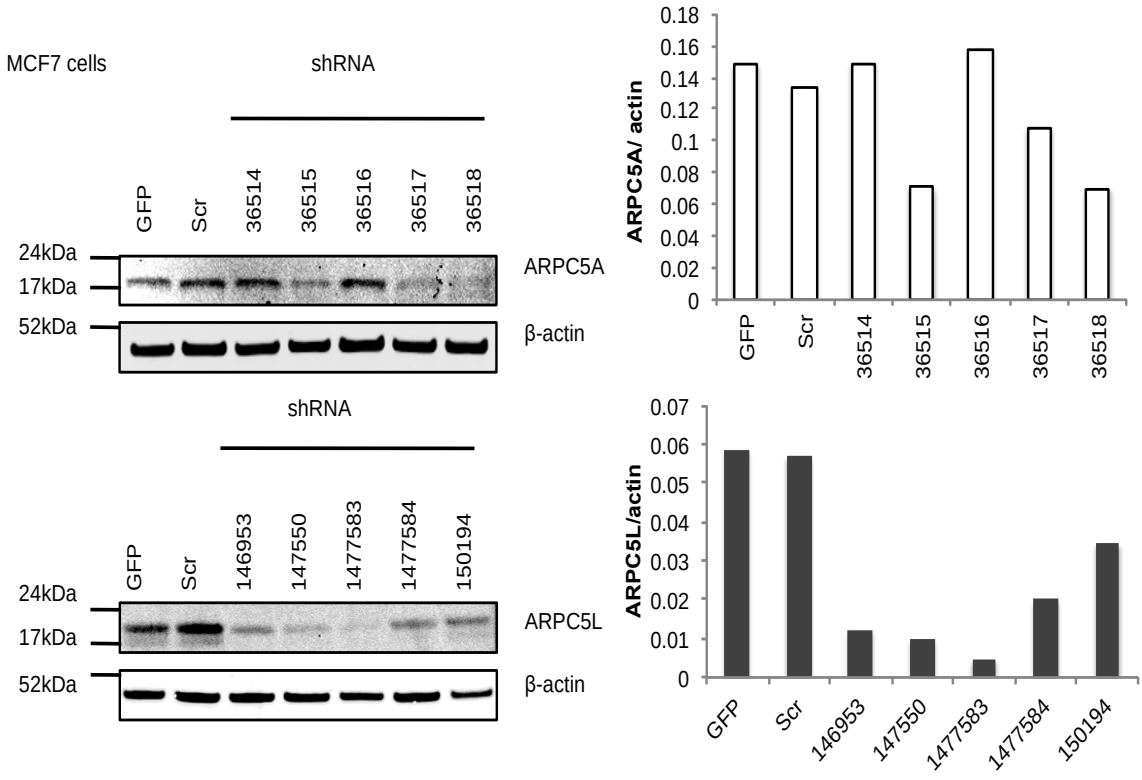


Figure 35: Knockdown of ARPC5A and ARPC5L in MCF7 cells with the use of different shRNA clones. MCF7 cells were infected by different shRNA clones from the Sigma MISSION® library as well as GFP and scrambled sequence (Scr) controls. Western blot and densitometry analysis of the protein levels of ARPC5A and L after two weeks of puromycin selection (n=1).

5.2.10. Morphological changes in MCF7 cells expressing reduced levels of ARPC5A and L

To perform this analysis, I chose the shRNA infected MCF7 cell lines which had effective knockdown of ARPC5A and L in combination with high viability (clones 36518 for ARPC5A and 146953 for ARPC5L (from Figure 35). Figure 36 shows that ARPC5A knockdown caused MCF7 cells to acquire a “spikey” appearance characterised by pointed membrane protrusions. ARPC5A knockdown cells also appeared smaller in comparison to control cells. In contrast, ARPC5L knockdown induced MCF7 cells to take on a more flattened and stressed morphology.

Additionally, cultures of ARPC5L knockdown cells seemed to be sparsely populated compared to control and ARPC5A knockdown cells, suggesting ARPC5 could have a role in cell cycle progression. This was investigated in the next section.

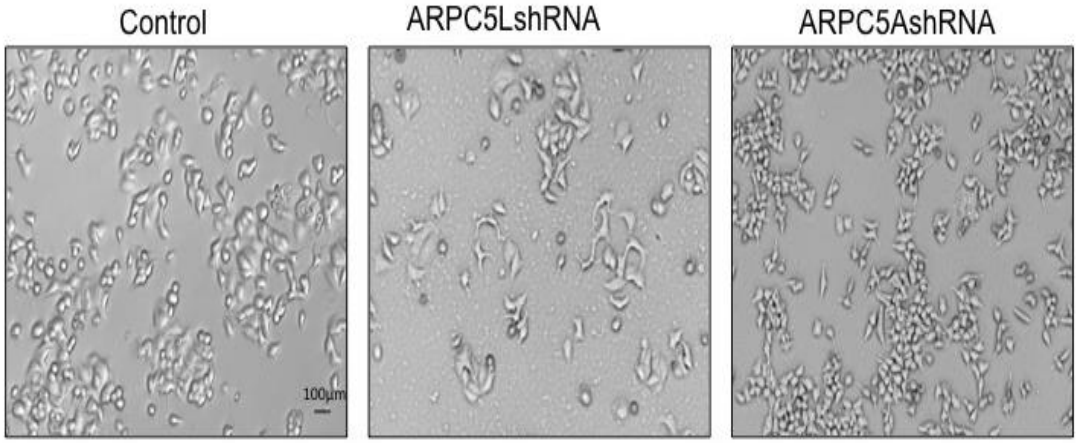


Figure 36: Morphology of MCF7 cells treated with shRNA against ARPC5A and ARPC5L (clones 36518 for ARPC5A and 146953 for ARPC5L, Sigma MISSION® library). Morphological changes were observed in MCF7 cells treated with shRNA against ARPC5A 16 days after infection with the viral vectors.

5.2.11. Effect of knockdown of ARPC5A and L by short hairpin RNA-mediated gene silencing on MCF7 cell proliferation.

To investigate the effect of ARPC5A and L knockdown on MCF7 cell proliferation I measured BrdU incorporation during DNA synthesis by using an ELISA-based BrdU incorporation assay (Roche,UK) as described in 5.1.4.

I found that MCF7 cell proliferation was weakly correlated with the expression of ARPC5A where proliferation of MCF7 cells infected with various shRNA clones to reduce ARPC5A expression the R^2 was 0.50595 (Figure 37). ARPC5L knockdown also affected MCF7 cell proliferation, but this seemed to be shRNA clone-specific rather than an effect that was related to protein expression (R^2 of the relationship between MCF7 cell proliferation and ARPC5L expression was 0.061620). For example, clone 583 profoundly inhibited MCF7 proliferation in line with its ability to reduce ARPC5L expression. In contrast, clone 194 had similar effects on cell proliferation but was not as effective at knocking down ARPC5L expression. Clones expressing GFP or the scrambled (Scr) shRNA control were used as a negative control.

The reasons for this discrepancy are not clear but could be related to the ability of each shRNA clone targeting ARPC5L to induce a flattened-stressed morphology on MCF7 cells. The clone 583 imposed this morphology but 194 did not.

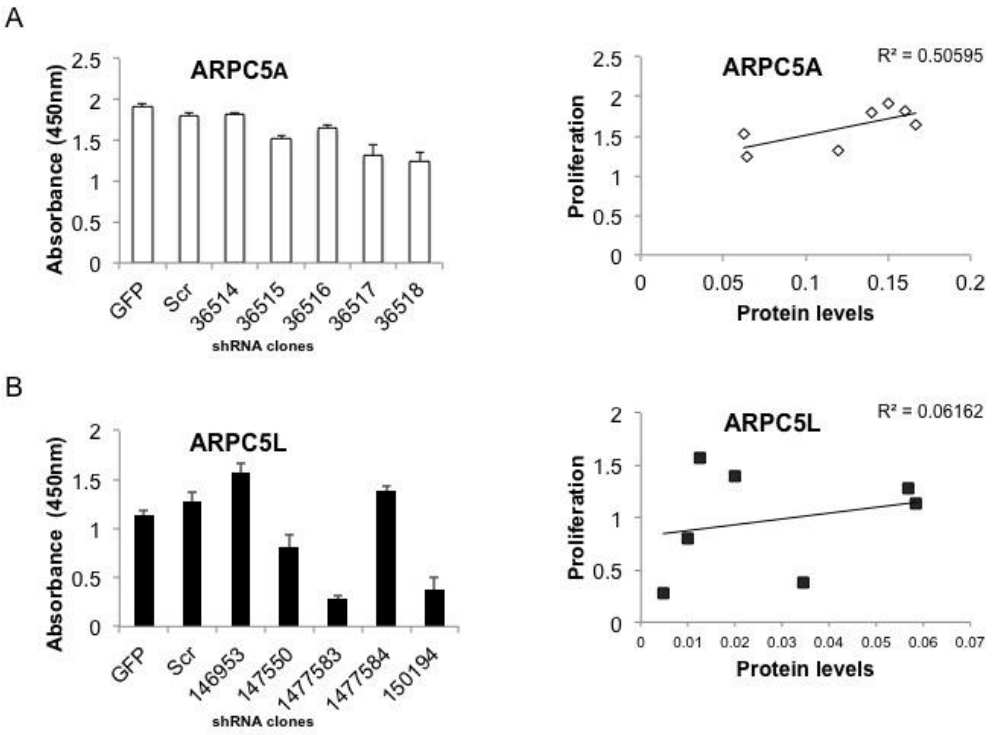


Figure 37: Proliferation rate of MCF7 cells measured by BrDU assay does not have a strong correlation with levels of ARPC5A or ARPC5L, infected with different shRNA clones targeting ARPC5 paralogs: Triplicates of MCF7 cells, transfected with different shRNA clones targeting ARPC5 paralogues, were incubated with BrdU labelling reagent. Cells infected with scrambled-shRNA control or GFP served as negative control. Error bars refer to triplicates within the same experiment. A. Proliferation rate of MCF7 cells transfected with control and ARPC5AshRNA clones and correlation between degree of knockdown and proliferation rate (R^2= 0.50595). B. Proliferation rate of MCF7 cells transfected with control and ARPC5LshRNA clones and correlation between degree of knockdown and proliferation rate (R^2= 0.06162).

5.2.12. Study of expression of ARPC5 paralogues in CLL patients at different disease stages (Binet A or Binet B/C)

One of the main findings of this study is the discovery of a role for ARPC5A and L in cell migration. My findings were observed in the cell lines MCF7 and MAVER-1 representing epithelial cells and B cells. ARPC5A and L expression may have consequence in particular malignancies (Figures 8, 22). CLL is one disease that appeared to have predominant expression of ARPC5L suggesting, that in this disease this predominance may be pathophysiologically important. This could play a role in understanding lymphadenopathies in progressive CLL because the malignant cells of this disease transit these proliferation centres only very slowly (188).

To address ARPC5A and L expression in primary CLL cells I used samples from a cohort of well-characterized patient samples (a kind gift from Dr David Allsup, University of Hull). Tables 10 and 11 (Appendix) list the cohort of patient samples used and some of their clinical characteristics relevant to this study. For the purposes of this investigation, I compared the ratio of ARPC5L/A expression in CLL cells from Binet stage A patients with Binet stage B/C patient samples (Table 10,11). I looked at Binet staging as one of its defining parameters is the presence of lymphadenopathy (189). Lymphadenopathy is relevant to this study as CLL cell migration to lymphonodes provides protection from chemotherapy and immunotherapy. Accessory cells such as T cells, mesenchymal stromal cells, and nurse-like cells constitute a protective microenvironment where apoptosis can be prevented and clonal proliferation can be supported within specific structures (190).

Figure 38 shows that CLL cells from Binet stage A patients appear to have a higher ARPC5L/A ratio than did cells from CLL patients with lymphadenopathy however there is not enough evidence for a 5% confidence level ($\chi 2=2.95$, $p=0.086$), Notably, levels of ARPC5 paralogues exhibit greater variation compared to levels of ARPC2 in this patient cohort.

The aim of this experiment was to test whether CLL cells containing high levels of ARPC5L had the potential to transit proliferation centres rapidly, whereas

CLL cells containing low levels of ARPC5L would be retained leading to the development of lymphadenopathy. This hypothesis was based on observations where ARPC5A and L protein expression is manipulated in MAVER-1 cells. Nevertheless, despite an intriguing trend, no relationship was found between ARPC5 paralogue expression in CLL cells and lymphadenopathy in the cohort I looked. However as this could be potentially interesting observation, further experiments within a larger cohort could have been performed.

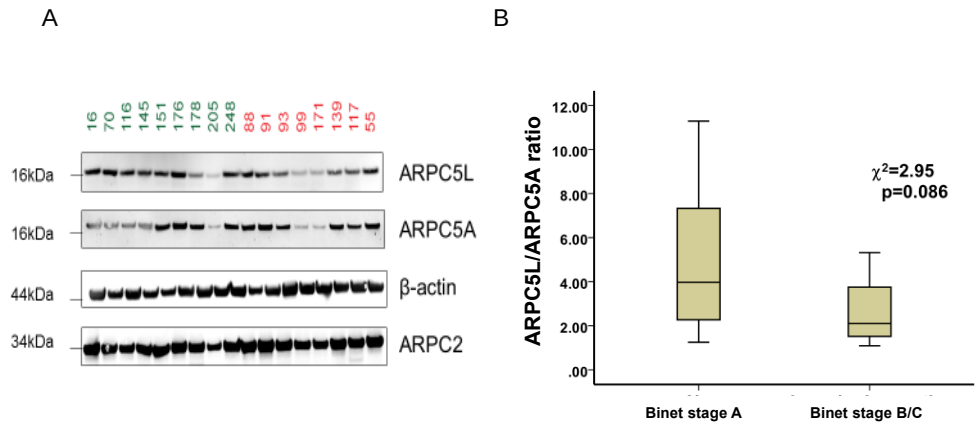


Figure 38: Investigation of the role of ARPC5L/ARPC5A protein expression ratio in CLL cases stratified in two different subgroups (Binet stage A and Binet Stage B/C). Lysates from 17 primary CLL cases, stratified based on clinical staging were analyzed on a 20-well NuPAGE™ 4-12% Bis-Tris Midi Protein Gels for levels of ARPC5A and ARPC5L (n=1). B. Box and whiskers plot representing the ratios of ARPC5L/ARPC5A protein expression in the two groups of CLL patients (Binet stage A, Binet stage B/C).

5.2.13. Analysis of migratory capacity of primary CLL cells.

Whilst the above studies of ARPC5L/ARPC5A expression ratios in primary CLL cells did not seem to yield a statistically significant result linking ARPC5 paralog expression to clinical staging, my results in MAVER-1 cells coupled with a trend observed in the data in Chapter 5.2.12 ($p=0.086$) lead to further investigation of chemokine-induced migratory capacity in the characterized CLL cell clones (performed by Dr Kathy Till).

For this experiment the chemokine CCL21 was used as chemotactic agent because of its ability to trigger in vitro chemotaxis of CLL cells (191). Figure 39 shows that CLL cells from Binet stage B/C patients show a trend to migrate towards chemokine despite BCR engagement ($p=0.061$), whereas CLL cells from Binet stage A cases tend to arrest following BCR engagement.

Following the completion of this study, future experiments will aim to explore a relationship between ARPC5L/ARPC5A expression and disease in CLL particularly with respect to the pathogenesis of lymphadenopathy in this disease.

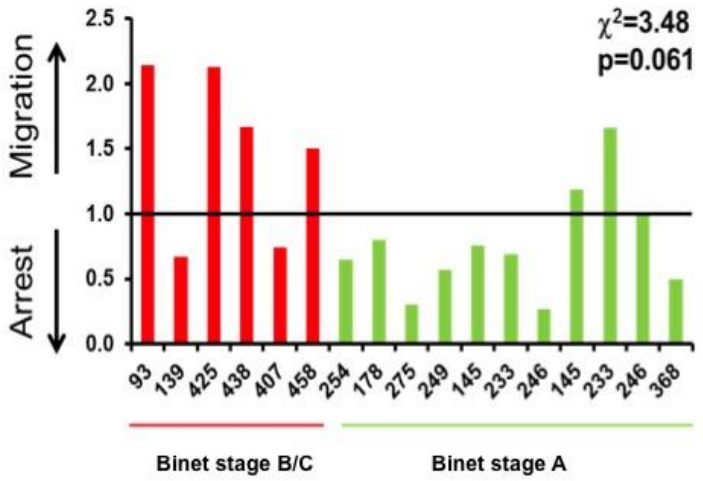


Figure 39: ARPC5L/A expression and migratory capacity of primary CLL cells. 1x10^6 CLL cells were seeded in to the top vessel of a transwell plate in the presence or absence of 20 µg/ml F(ab')2 fragment. In the bottom well CCL21 1mg/ml was included to induce chemotaxis. After 4 hours cells were harvested form the bottom well and migration index determined by counting the number of CD19+ cells. Migration or arrest was determined as the ratio of migration index between untreated and BCR crosslinked CLL cells. Values greater than 1 indicate migration despite BCR crosslinking, values less than 1 indicate migration arrest in the presence of BCR crosslinking. Statistical analysis was performed using a Fisher's exact test. This experiment was performed by Dr Kathy Till.

5.3. Discussion

In this chapter, I investigate the functional role of ARPC5L and its paralog ARPC5A in MCF7 and MAVER-1 cells. A principal finding is the relative roles that ARPC5A and L play in facilitating cell migration in cell line models. Thus,

reduction of ARPC5A expression or overexpression of ARPC5L appear to enhance the ability of cells to migrate. This observation may be related to knockdown induced phenotypical changes: knockdown of ARPC5A generated a spiky phenotype in MCF7 cells whereas knockdown of ARPC5L expression did not affect cell migration but seemed to alter the phenotype of MCF7 cells, which became flattened and stressed under these conditions. Interestingly, knockdown of ARPC5L in B cells also seemed to affect cytoskeleton by blocking the ability of BCR to polarize actin filaments

These results show a common pattern of migration capacity between two different cell types (MCF7 and MAVER-1) when levels of ARPC5A and L expression are altered.

ARPC5L was first identified in 2003 in a study that reported its sequence and tissue distribution. Originally designated ARPC5B it was recognized as a paralog of ARPC5A (123). These proteins are known components of the ARP2/3 complex and have recently been shown to play important roles in actin dynamics (134).

The ARPC5A and ARPC5L proteins largely share similar expression pattern except in brain where ARPC5L is more highly expressed and spleen where ARPC5A appears more highly expressed. In this study by Machesky et al, it is mentioned that ARPC5A is enriched in tissues that contain high levels of blood cells and is present at relatively high levels in neutrophils and lymphocytes, suggesting that high levels of ARPC5A may be particularly associated with cells of haematopoietic origin (123). However, no data is presented on the cellular role of the ARPC5 isoforms or the mechanisms that control their expression. The only report of the ARPC5L isoform in B cells was in 2008 where a gene expression profile study was performed to identify genes that were modulated upon BCR stimulation in CLL cells. ARPC5L was within the genes that were significantly upregulated in UM-CLL cases upon BCR stimulation (84). This work identifies upregulation of ARPC5L as an event that could play a role in CLL disease progression but offers no functional explanation for its role.

One of the principal findings in this chapter has been the observation that ARPC5A knockdown facilitates cell migration. This was first noticed in MCF7 cells and validated with two different assays. During the knockdown studies, a paralogue compensation mechanism was observed; implying that higher expression of the L isoform over A was responsible for the changes in cell migration. This observation was confirmed with the ARPC5A and L ectopic expression experiments in MCF7 cells leading us to conclude that in this cell line a high ARPC5L/ ARPC5A expression ratio facilitates migration, whereas high levels of ARPC5A to L do not affect or may even impede migration.

Due to the focus of this study on B cell biology, I attempted to test these observations in a B cell system. In the MAVER-1 cells, a transwell migration assay showed that ARPC5A knockdown cells migrate faster to the bottom of the well compared to cells with reduced ARPC5L expression. In the same assay , I noticed that MAVER-1 cell migration to CXCL-12 and CCL21 is arrested when BCR is crosslinked, an observation that is in keeping with a previous study (186). BCR arrest of chemokine-induced migration in our system is not mediated by changes in expression of the receptor for CXCL-12, as suggested by Guinamard et al, because my experiments showed that BCR crosslinking on MAVER1 cells did not reduce CXCR4 expression on these cells. The reasons for this are unclear but may be due to differences in cell systems used.

Previous studies have shown that, at a functional level, the Arp2/3 complex has an essential role in lamellipodia-mediated cell migration by generating branched actin filament networks (134) In addition, the discovery of different isoforms for Arp2/3 subunits has lead to the observation that the cell migration rate can be isoform-specific in a *Vaccinia* virus model system. In particular, ARPC5 isoforms affect Arp2/3 complex-mediated actin filament assembly as well as the disassembly of branched actin filament networks. Interestingly, complexes containing ARPC5L are more efficient at nucleating actin filaments and are also better shielded against actin disassembly (134).

In migrating cells, the molecular mechanisms of actin polymerisation in membrane protrusions have been associated with the ability of cells to migrate

(192). In CLL, entry of malignant cells in the lymphnodes as well as exit (or egress) is central to the physiology and manifestation of the disease (88). However, the link between actin dynamics and CLL cell migration has not been completely elucidated.

Most observations about CLL cell migration have focussed on the CXCR4/SDF-1 axis. Therapeutically, a CXCR4 antagonist AMD3100 has been described to interfere with CLL cell migration by inhibiting cell response to SDF-1 as well as actin polymerization (193). Potentially, ARPC5A and L could function together with HS1, a homologue of cortactin that is known to be a link between the cytoskeleton and BCR signalling. By interacting with actin and the Arp2/3 complex, HS1 is involved in cytoskeleton modifications and in the assembly of actin filaments (194). When Lyn activates HS1 in a subset of CLL patients, there is an increase in cytoskeletal functionality in terms of migration and F-actin polymerization. Phosphorylation of HS1 is generally higher in poor-prognosis patients (106) and therefore is considered a potentially significant player in CLL. HS1, like cortactin, has an affinity for the Arp2/3 complex and could conceivably also interact with ARPC5L and ARPC5A. The results presented in this chapter show that ARPC5L/ARPC5A expression ratios vary in CLL patient cells. Expression ratios were used instead of manipulating ARPC5L and A expression because of the technical difficulty of a 72 h siRNA knockdown in CLL cells. Although levels of expression could not be correlated to the presence of lymphadenopathy in patients, it is intriguing to speculate that these expression ratios may be the result of BCR-induced changes to ARPC5 paralog expression because CLL cells derived from patients with lymphadenopathy have evidence of exposure to BCR engagement (195). Proof of this speculation will require further work.

Based on these results, Dr Kathy Till I decided to look at ARPC5L/ARPC5A expression in relation to CLL cell migration (Chapter 5.2.13). The hypothesis was that cells with low ARPC5L/ARPC5A expression ratios do not arrest in response to BCR crosslinking, and that CLL cells with this phenotype are likely to maintain movement within lymphnodes, albeit slow movement, and this results in lymphadenopathy. On the other hand, CLL cells with high

ARPC5L/ARPC5A ratios are likely to traffic through lymphnode environments without hindrance. To prove this Dr Till performed migration assays in a cohort of CLL cases categorised according to Binet stage. A direct relationship between CLL cell migration and lymphadenopathy could not be shown, but further work may be necessary because there are studies that show BCR crosslinking enhances CLL cell migration to chemokine (196), while there are others that suggest such crosslinking arrests chemokine-induced migration (197). There are other factors that are associated with nodal presentation in CLL such as CD49d (reviewed in (198)), an integrin whose activation involves both BCR and chemokine receptors, and the receptor for sphingosine 1-phosphate whose expression is controlled by BCR engagement (199). If further studies confirm a correlation between clinical staging and migration for our cohort, ARPC5 paralog levels will be analysed.

Taken together, our data highlights the role of the ratio of ARPC5 paralogs for the migration of B lymphocytes.

6. Discussion

BCR engagement activates signalling pathways essential to the behaviour of normal and malignant B-cells. As such BCR signalling contributes to proliferation, survival and induction/suppression of differentiation in normal and malignant B cells (12,195). At the beginning of this study, there were no reports of global approaches attempting to dissect active BCR signalling, and construction of our understanding was based on Western blot and phosphoflow (200) technologies to detect target epitopes. However, although these methods are effective, they are subject to limitations such as hypothetical targets, lack of detection sensitivity and ability to measure more subtle changes in signalling pathways when the frequencies or magnitude of response are very low (201). These limitations create a need for a different approach. For example, and for the purposes of this thesis, SILAC technology combined with mass spectrometry was used to analyze phospho-tyrosine signalling networks initiated by BCR signalling because of success in understanding similar networks in other cells stimulated with EGF and PDGF (171,202).

The main aim of this thesis was to provide insight into active phosphorylation pathways of malignant B cells, and further explore any novel findings revealed by analysis of the phosphoproteomic dataset generated by BCR engagement. I found 854 proteins within the JeKo-1 cell anti-pTyr immunoprecipitate, seven percent of which showed differential presence within BCR-stimulated compared to unstimulated cells. Specifically, 35 proteins were significantly over represented, whereas 25 were underrepresented, and these proteins were all classified as those responsive to BCR stimulation. Performing Gene Ontology (GO) term enrichment analysis of the whole dataset confirmed the validity of my method by highlighting the BCR signalling pathway as a prominent group of differentially phosphorylated proteins. BCR signalling pathway proteins were also recognized when using the PANTHER database or the STRING resource for interaction data, providing further support for the validity of this method. Interestingly, PANTHER and STRING also revealed

cytoskeletal proteins among the BCR responsive proteins, and, in particular, members of the Arp2/3 complex.

In depth analysis of our data highlighted that 5 out of 7 proteins within the Arp2/3 complex increase within the group of BCR responsive proteins by more than 30%. In particular, the fifth most abundant protein in the BCR phosphotyrosine network is ARPC5L, a recently discovered paralog of the ARPC5A subunit of the Arp2/3 complex. Analysis of the peptide sequence of ARPC5L using the PHOSIDA and PhosphoSitePlus databases (203,204) (Figure7) revealed that this protein did not contain tyrosine residues within consensus phosphorylation sites of known tyrosine kinases. In this study I used phos-Tag gels to look at the phosphorylation status of ARPC5L, but was not able to observe a reproducible mobility shift (chapter 1.x). Nevertheless, the existing information on ARPC5L phosphorylation status suggests that representation of ARPC5L within the group of BCR responsive proteins is not because it is directly phosphorylated. More likely, ARPC5L is associated with tyrosine phosphorylated proteins, in a stimulation-dependent manner, the nature of which remains undefined within this thesis. Potentially, proteins co-associating with ARPC5L could be cortactin as is already described for the Arp2/3 complex (205) or a homologue of cortactin such as HS1 (206). Both cortactin and HS1 are substrates of tyrosine kinases within cells (207). ARPC5L has also been identified in a PKD2 (Protein Kinase D2) protein interaction network study in HeLa cells where chemical crosslinking is used to capture direct protein-protein interactions. The relevance of this observation to the current study is that PKD2 is a serine and threonine kinase that is found to be autophosphorylated in reactive lymphnodes and lymphoid tumours.

The molecular function of the Arp2/3 complex is the regulation of actin polymerization (111). Activation of this complex occurs through interaction with nucleation-promoting factors such as WASP, N-WASP and cortactin, all of which can bind the complex directly (118). In haematopoietic lineage cells the cortactin homologue HS1 can also bind the Arp2/3 complex with similar efficiency as cortactin, but may not have the same ability to facilitate formation of branched actin chains due to less affinity than cortactin for the binding of F-actin (206). HS1 is phosphorylated at tyrosine residues upon activation of the

BCR. Specifically, Syk can phosphorylate HS1 on tyrosines 378 and 397 and generate binding sites for Src family kinases. This leads to secondary phosphorylation of HS1 on tyrosine 222 by these kinases (208). In neutrophils, tyrosine phosphorylation of HS1 is important for enhancing its interaction with the Arp2/3 complex and facilitating chemotaxis (107). In CLL cells it is proposed that LYN phosphorylates HS1 on tyrosine 397, and it is demonstrated that such phosphorylation correlates with bad prognosis and also with increased cytoskeletal functionality in terms of lymphocyte migration and chemotaxis (194). Association of HS1 and ARPC5L was not observed in the experiments presented in this thesis because of technical difficulty in identifying ARPC5L co-immunoprecipitating with HS1. ARPC5L migrated very close to Ig light chain in SDS-PAGE gels making it difficult to identify this protein by Western blot. Furthermore, the antibodies available to us were poor with respect to immunoprecipitating ARPC5L. Nevertheless, it is an attractive hypothesis that pHS1 associates with ARPC5L given the evidence showing induction of HS1 phosphorylation by BCR crosslinking and the role such phosphorylation plays in association of HS1 with the Arp2/3 complex.

Active Arp2/3 regulates cytoskeletal dynamics within cells, and a principal biological process that depends on rearrangement of cytoskeletal elements is cell migration (209). For the purposes of this thesis I initially used MCF7 cells, a breast cancer cell line, because of established assays to measure cell movement and for their suitability for siRNA experiments. I conclude from this model cell line that ARPC5L/ ARPC5A expression ratios affect migration of cells as measured within a wound healing assay as well as tracking individual cells as they migrate on a microscope slide. Interestingly, knockdown of ARPC5L led to increased levels of ARPC5A, and vice versa, respectively decreasing or increasing the ARPC5L/ARPC5A ratio. Potentially this apparent compensation of isoform expression points at diversity in function of the two paralogues despite their sequence homology. I found that predominant expression of ARPC5L (when expression of ARPC5A is reduced by siRNA) enhanced cell migration, whereas predominant expression of ARPC5A had little, if any, effect. I was able to transfer the results observed using MCF7 cells to the B-cell line model (MAVER-1 cells). In transwell migration assays to

measure chemokinesis I found that ARPC5A knockdown in MAVER-1 cells results in faster migration of the cells. Like MCF7 cells, reduction of ARPC5L expression in MAVER-1 cells did not largely affect migration of the cells when they were exposed to chemokine. Taken together, these experiments show that ARPC5A and ARPC5L function in a similar fashion between cells of different origin, MCF7 cells are epithelial in origin (210) whereas MAVER-1 cells are mesodermic in origin (146). My results in these two different cell systems, agree with the findings of Way et al. who describe the role of these paralogues within the Arp2/3 complex using a model of actin-based motility of *Vaccinia* virus (134). According to this report, Arp2/3 complexes containing ARPC5L are more efficient in promoting actin polymerization than those containing ARPC5A. In addition, cortactin preferentially stabilizes Arp2/3 complexes containing ARPC5L over complexes containing ARPC5A against coronin-mediated debranching. These findings are likely applicable within the migration assays I performed in this thesis, but require further investigation because the mechanism through which ARPC5 paralogs differentially regulate cell migration is not elucidated.

My findings provide insight into the regulation of cytoskeletal dynamics following BCR engagement. Such engagement is known to arrest B cell chemokinesis (80), and the results presented in this thesis using MAVER-1 cells and CXCL12 and CCL21 support this paradigm. Although both spontaneous and CXCL12-induced migration of MAVER-1 cells is enhanced by knockdown of ARPC5A, BCR crosslinking reduced this migration in a similar way as was observed in control transfected cells. In contrast when performing these experiments having knocked down ARPC5L, cells did not respond to addition of the chemokine by enhancing migration, possibly due to the reduced ability if ARPC5L to organise the cytoskeleton and BCR crosslinking seemed to induce migration.

That BCR engagement arrests B-cell chemokinesis suggests that BCR engagement has predominance of command over chemokine receptor with respect to the cytoskeletal dynamics involved in BCR-mediated processes

(receptor internalization, cell spreading etc.) versus chemokine receptor induced migration. With regards to ARPC5L, the fluorescence microscopy experiments included in this thesis suggest a role for ARPC5L in this command. Here, it is apparent that knockdown of ARPC5A has no effect on the ability of BCR to organize actin. However, this ability is inhibited by knockdown of ARPC5L. Thus, I hypothesised that in the absence of ARPC5L and ability to organize cytoskeleton BCR–stimulated cells would be able to migrate towards chemokine. This hypothesis could have interesting implications regarding the different mechanisms in the way chemokine and BCR engagement induce cytoskeletal rearrangement and could justify why ARPC5L is highly represented within the set of BCR responsive proteins identified by the phosphoproteomic experiments. However, I was not able to solidly establish a link between my protein of interest and the relationship bwtween BCR stimulation and chemotaxis his by the migration experiments in BCR stimulated MAVER-1 cells, as I knockdown of ARPC5L seemed to stop the cells from moving towards CXL12. BCR engagement commands ARPC5L functionality, whether this command involves HS1 phosphorylation and association with ARPC5L requires further investigation.

B cell spreading was investigated as it represents a link between BCR signalling and the actin cytoskeleton, a link that also appears in our proteomics data (211,212). Batista and others have shown that spreading is important for the immune functioning of B cells. When the BCR is stimulated through contact with membrane-bound antigens, B cells begin to spread (in an F-actin dependent way) to form the immune synapse, prolong BCR signalling, improve antigen internalization, and facilitate microcluster-formation to allow additional BCR complexes to bind antigens (100,213). My findings show that knockdown of ARPC5A and L does not affect the ability of MAVER-1 cells to spread on IgM-coated coverslips, however we were able to observe a difference in the organization of the cytoskeleton when the L paralog is knocked down. Recent work targeting the role of Arp2/3 complex in BCR signalling suggests that this complex is essential for actin structural organization during cell spreading (214). The work presented in this thesis refines this finding to identify a key player, ARPC5L, within the process of BCR-mediated actin structure

organization.

My findings provide insight into B-cell trafficking. Mature B-lymphocytes in the blood constantly move between this media and the tissues of secondary lymphoid organs such as spleen and lymph nodes in their quest for cognate antigen (215). Entry of cells into lymphnodes is controlled by the action of chemokines, principally CCR7 ligands, and then B cells move between T-cell rich areas and the follicle (216). If cells fail to recognize antigen then a process of egress is initiated whereby the receptor for sphingosine-1-phosphate (S1PR1) is reexpressed and cells move out of the lymphoid tissue according to a gradient of S1P (217). However, if B cells encounter antigen, they are retained in secondary lymphoid organs to undergo clonal expansion and differentiation to either memory B cells or antibody producing plasma cells (218). Part of the differentiation process involves induction of expression of human germinal centre-associated lymphoma protein (HGAL), a protein demonstrated to limit lymphocyte motility (spontaneous and chemokine-induced) through activation of the RhoA signalling pathway (219). My findings provide insight into migration arrest that is proximal to the induction of HGAL, in our experiments migration arrest was an immediate result of BCR crosslinking and was not due to changes in expression of chemokine receptor or of expression of HGAL, the latter requiring co-stimulation of B cells with CD40 ligand and IL-4 (99).

My observations concerning lymphocyte trafficking are potentially important for B cell lymphomas. In contrast to normal B cells, the lymphocytes of B-cell lymphomas mostly reside within lymphoid tissues (220). Releasing the malignant cells from their protective microenvironment limits their access to stimuli required for their growth and survival (221). Therefore, the mechanisms that control migration arrest have emerged as an important therapeutic route for this category of blood cancers. In particular, CLL has been extensively studied with regard to cell motility and trafficking, leading to the establishment of relevant prognostic factors in recent years such as expression of integrin $\alpha 4$ (222). In agreement with these findings, clinically successful drugs targeting BCR components have been shown to also target CLL cell trafficking. When

administered to CLL patients, the PI3Kδ inhibitor idelalisib (CAL-101), the SYK inhibitor fostamatinib and the BTK inhibitor ibrutinib all produce lymphocytosis and lymphnode size reduction through their ability to release CLL cells from their protective environment (220). The mechanisms through which this is achieved is through regulation of chemokinesis and ligand binding, by integrins (Ibrutinib, Fostamatinib) (223,224), or promotion of cell egress (Idelalisib) (225). In this study, I looked at the ARPC5L/ARPC5A ratio of primary CLL cells grouped according to physical findings of splenomegaly and lymphadenopathy concurrent with disease stage.

My hypothesis was that Binet stage A patients would tend to have a higher ARPC5L/ARPC5A ratio compared to Binet stage B or C patients. However, I was not able to observe a strong correlation between ARPC5L/ARPC5A ratio of the studied CLL cases and clinical staging. This could be due to expression of other proteins which are strongly associated to lymphadenopathy such as CD49d (226), an integrin of which the expression is decreased by different CLL drugs.

Whilst the focus of this thesis has been the findings in B cell lines another line of research could arise from this work, aiming to translate these findings to clinical CLL samples, thereby pointing at a possible mechanism to explain lymphadenopathy within the pathophysiology of CLL. Additional experiments were performed by members of the CLL group to look at the migratory capacity of CLL cell clones from different clinical groups towards chemokine. Future studies will look at the ARPC5L/ARPC5A ratio in these cases to test whether there is a link with CLL cell migration. The basis for these experiments comes from studies demonstrating evidence of BCR engagement in CLL cells from patients with lymphadenopathy (227). The current study did not address how expression of ARPC5L and A is regulated within cells. It is conceivable, based on potential ubiquitination sites within ARPC5L, that long term BCR engagement may suppress expression of this protein by facilitating its destruction within the proteasome (228). Whether this is indeed the case requires further investigation that is outside the scope of this thesis.

One of the inherent limitations of our experimental design was the use of a cell line to model primary B cells. Cell lines are commonly used to model tumour behaviour *in vitro* to dissect molecular mechanisms, to establish drug sensitivity and to identify biomarkers of disease (229). The quest for an optimal cell line model for each study has been aided by the accumulation of data to characterize cell lines in databases such as the Cancer Genome Atlas (TCGA), The Broad-Novartis Cancer Cell Line Encyclopaedia (CCLE), and the International Cancer Genome Consortium (ICGC) (230,231). In this thesis, I required a B cell line, which mimics CLL cell signalling, and also resembled the CLL cell phenotype. A number of cell lines derived from CLL and other B cell malignancies were identified and investigated for their responses to BCR crosslinking and sensitivity to known CLL signalling inhibitors. In addition, I looked at surface marker expression, testing the cell lines for similarity to a CLL cell phenotype. According to my findings Jeko-1 cells/MAVER-1 cells, mantle cell lymphoma cell lines, were found to best fit the set criteria but also fulfil one of the practical requirements of this study which was an ability to proliferate in SILAC medium. These MCL cell lines are different from CLL cells with respect to expression of the BCR, the former cells express much more of this receptor than the latter cells (232,233). Moreover, Jeko-1 and MAVER-1 cells are fully competent to respond to BCR engagement, whereas CLL cells retain elements of BCR anergy (234). It is therefore probable that the phosphoproteomic analysis of BCR signalling in JeKo-1 cells does not completely model that which occurs in CLL cells. Nevertheless, such analysis recapitulated proximal BCR signalling events in CLL cells as it is currently understood within the literature (235).

In conclusion, I demonstrate a role for ARPC5 isoforms in B lymphocyte migration, and provide insight into their pathophysiological roles in B cell malignancies. My data led me to investigate a link between BCR signalling and cytoskeletal rearrangements associated with migration. If this finding is proved by further experiments it could potentially be clinically important because of the predominant expression of ARPC5L and role of BCR in malignant B cells in several diseases. An exact mechanistic role for ARPC5 isoforms is not revealed by the experiments performed in this study, however

the isoform specific functional differences I did find provide the groundwork for further exploration of Arp2/3-controlled cytoskeletal events in B cells to give further information of the pathophysiology of CLL cells.

7. Appendix

For the functional studies to investigate the role of ARPC5 paralogues performed in this project I used the mantle cell lymphoma cell line, MAVER-1 (146). In order ensure the similarity of MAVER-1 cells to CLL as well as their compatibility to JeKo-1 cells that were used for the proteomics part of study, I characterized the MAVER-1 cells for surface marker expression as well as their signalling response to BCR stimulation. According to Figure 41 A, MAVER-1 cells, similarly to JeKo-1 and CLL, express CD5, CD20 and surface IgM. MAVER-1 cells also seem to have low levels of global pY which are induced when the BCR is crosslinked (Figure 40 B),

In addition, Figure 22 shows that MAVER-1 cells like JeKo-1 and CLL are characterized by a high ARPC5L/ARPC5A ratio in comparison with other cell types, thus making this cell line a suitable tool to draw meaningful functional conclusions.

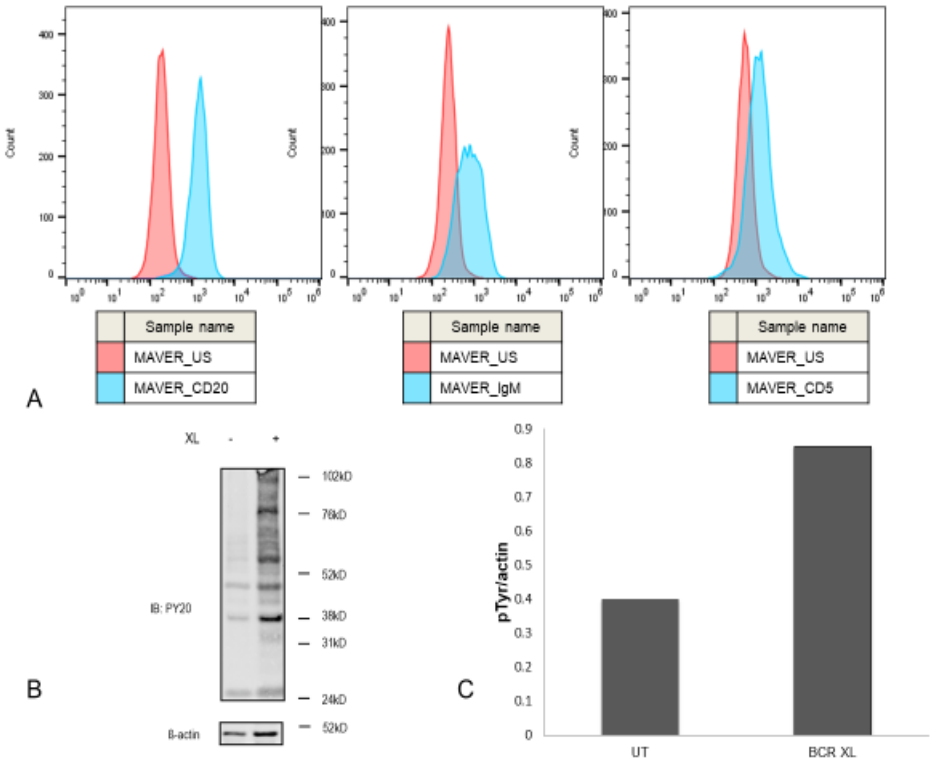


Figure 40: Characterization of MAVER-1 cells. A. MAVER-1 cells ($1x10^6$) were stained with mAbs to detect expression of CD20, CD5 and sIgM (BD Biosciences) or isotype control, the staining was measured by FACS analysis using a FACSCalibur™ instrument. B. Western blot for the analysis of MAVER-1 cell lysates (20 µg) for levels of PY20 (Santa Cruz Biotechnology, Inc, Heidelberg, Germany) +/- BCR stimulation. C. Densitometry analysis for blot (n=1)

Sample ref	WBC	Karyotype
16	77.3	Normal
70	38.3	Normal
116	57	Normal
145	68.4	Normal
151	44.3	Normal
176	27	Normal
178	28	Normal
205	60.8	Normal
248	20.5	Normal
88	211.3	13q del
91	138.7	Normal
93	37.1	13q del
99	42.1	Normal
171	214	Normal
139	106	Normal
117	26.8	13q del
55	277	Normal

Table 11: Characterization of 18 clinical CLL samples used in this study based on White Blood cell Count (WBC) and fluorescence in situ hybridization (FISH) analysis. Samples depicted in green are Binet stage A, whereas samples depicted in red were diagnosed as Binet stage B/C.

Supporting information

Supplementary Tables 1 and 2 attached to this thesis in a CD, contain the raw data from the phosphoproteomics experiment in Chapter 4 and the technical replicate experiment (Chapter 4.6.1).

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Ptyr network of BCR signalling in JeKo-1 cells following 15 minutes of anti-IgM stimulation Peptides have been sorted based on log2 Heavy/Light ratio. Proteins highlght

Gene name			Protein descritpion	Peptide counts (	Peptide counts (	Peptide counts (	Proteins	Peptide	Razor + un	Uniqu
DMD	DMD	DMD Is	DMD Isoform 4 of Dystrophin;>IPI:IPI00472316.2|T	1;1;1;1;1;1	1;1;1;1;1;1	1;1;1;1;1;1	6	1	1	1
PLUNC	PLUNC	PLUNC	PLUNC Protein Plu	5	5	5	1	5	5	5
LYZ	LYZ	LYZ Lys	LYZ Lysozyme C	1	1	1	1	1	1	1
LCN1	LCN1	LCN1 Li	LCN1 Lipocalin-1;>IPI:IPI00176710.5|SWISS-PROT:Q	2;2	2;2	2;2	2	2	2	2
AZGP1	AZGP1	AZGP1	AZGP1 alpha-2-glycoprotein 1, zinc precursor;>IP	2;1;1;1	2;1;1;1	2;1;1;1	4	2	2	2
SF3B2	SF3B2	SF3B2 ;	SF3B2 splicing factor 3B subunit 2;>IPI:IPI00477	3;3	3;3	3;3	2	3	3	3
PIP	PIP	PIP Pro	PIP Prolactin-inducible protein	4	4	4	1	4	4	4
ZG16B	ZG16B	ZG16B	ZG16B Zymogen granule protein 16 homolog B	3	3	3	1	3	3	3
HSPE1	HSPE1	HSPE1	HSPE1 10 kDa heat shock protein, mitochondrial;>	2;2;1	2;2;1	2;2;1	3	2	2	2
AMY2A	#VALUE!	#####	#VALUE!	7;6;5;5;3;3;2;2	7;6;5;5;3;3;2;2	7;6;5;5;3;3;2;2	8	7	7	7
CTSD	CTSD	CTSD C	CTSD Cathepsin D;>IPI:IPI00853455.1|TREMBL:C9JIH	4;4;3;3;2;1	4;4;3;3;2;1	4;4;3;3;2;1	6	4	4	4
IGL@;IGI	#VALUE!	IGL@;I	IGL@;IGLV1-44;IGLV2-11;LOC100290481;IGLV1-40;IGL	2;2;2;2;2;2;2;1;1	2;2;2;2;2;2;2;1;1	2;2;2;2;2;2;2;1;1	24	2	2	2
NAGK				2;2;1;1	2;2;1;1	2;2;1;1	4	2	2	2
POLDIP3	POLDIP3	POLDIF	POLDIP3 cDNA FLJ54030, highly similar to Polymer	2;2;2;2;2;2	2;2;2;2;2;2	2;2;2;2;2;2	7	2	2	2
TPR				3	3	3	1	3	3	3
HNRNPR	HNRNPR	HNRNF	HNRNPR 71 kDa protein;>IPI:IPI00644055.3|SWISS-P	3;3;3;3;3;2	3;3;3;3;3;2	2;2;2;2;2;2	6	3	3	2
XRCC5	XRCC5	XRCC5	XRCC5 ATP-dependent DNA helicase 2 subu	10;3;2;1	10;3;2;1	10;3;2;1	4	10	10	10
HIST1H1	HIST1H1B	HIST1H	HIST1H1B Histone H1.5	6;2	6;2	6;2	2	6	6	6
SEPT2	SEPT2	SEPT2 I	SEPT2 Isoform 2 of Septin-2;>IPI:IPI00014177.3|S	6;6;6;5;3;3;3;3;3	6;6;6;5;3;3;3;3;3	6;6;6;5;3;3;3;3;3	17	6	6	6
GALK1	GALK1	GALK1	GALK1 cDNA FLJ56840, highly similar to Galactoki	3;3;2	3;3;2	3;3;2	3	3	3	3
SFRS7	SFRS7	SFRS7 I	SFRS7 Isoform 1 of Splicing factor, arginine/ser	4;4;4;4;2;1	4;4;4;4;2;1	3;3;3;3;2;1	6	4	4	3

PABPN1	PABPN1	PABPN	PABPN1 Isoform 1 of Polyadenylate-binding protei	1;1	1;1	1;1	2	1	1	1
XRCC6				12;12;11;10	12;12;11;10	12;12;11;10	4	12	12	12
SSRP1	SSRP1	SSRP1 I	SSRP1 FACT complex subunit SSRP1	2	2	2	1	2	2	2
SFRS1	SFRS1	SFRS1 I	SFRS1 Isoform ASF-1 of Splicing factor, arginine	7;6;6;3	7;6;6;3	7;6;6;3	4	7	7	7
GGCT	GGCT	GGCT	GGCT Isoform 1 of Gamma-glutamylcyclotransferas	5;4;3;2;1;1;1	5;4;3;2;1;1;1	5;4;3;2;1;1;1	7	5	5	5
CLNS1A	CLNS1A	CLNS:	CLNS1A Methylosome subunit pICln	2	2	2	1	2	2	2
HIST1H1(	HIST1H1	HIST1	HIST1H1C Histone H1.2;>IPI:IPI00217466.3|SWISS	6;5;5;1;1	6;5;5;1;1	6;5;5;1;1	5	6	6	6
PLD4	PLD4	PLD4 (	PLD4 cDNA FLJ56630, highly similar to Homo sapie	2	2	2	1	2	2	2
BAX	BAX	BAX Is	BAX Isoform Beta of Apoptosis regulator BAX;>IPI	2;2;2;2;2;1;1	2;2;2;2;2;1;1	2;2;2;2;2;1;1	7	2	2	2
NCL	NCL	NCL N	NCL Nucleolin;>IPI:IPI00444262.3|TREMBL:Q6ZS9	22;20;13;13;2;2;	22;20;13;13;2;2;	22;20;13;13;2;2;	7	22	22	22
TYMS	TYMS	TYMS	TYMS Thymidylate synthase;>IPI:IPI00103732.1|	2;2;2	2;2;2	2;2;2	3	2	2	2
ATIC	ATIC	ATIC E	ATIC Bifunctional purine biosynthesis protein PU	22;21;8;5;4;4;3	22;21;8;5;4;4;3	22;21;8;5;4;4;3	7	22	22	22
TSN	TSN	TSN T	TSN Translin;>IPI:IPI00917623.1|TREMBL:B3KRM8	7;7;5;3	7;7;5;3	7;7;5;3	4	7	7	7
THOC4	THOC4	THOC	THOC4 THO complex 4	6	6	6	1	6	6	6
FARSB	FARSB	FARSI	FARSB Phenylalanyl-tRNA synthetase beta chain	4	4	4	1	4	4	4
ADK	ADK	ADK Is	ADK Isoform Long of Adenosine kinase;>IPI:IPI002	2;2	2;2	2;2	2	2	2	2
GRPEL1	GRPEL1	GRPE	GRPEL1 GrpE protein homolog 1, mitochondrial;>IP	1;1	1;1	1;1	2	1	1	1
CBR1	CBR1	CBR1	CBR1 Carbonyl reductase [NADPH] 1;>IPI:IPI00795	6;3;3;2	6;3;3;2	6;3;3;2	4	6	6	6
NOLC1	NOLC1	NOLC	NOLC1 Isoform Beta of Nucleolar phosphoprotein p	3;3;3	3;3;3	3;3;3	3	3	3	3
TRIM28	TRIM28	TRIM2	TRIM28 Isoform 1 of Transcription intermediary f	7;6	7;6	7;6	2	7	7	7
HNRNPA	HNRNPA	HNRN	HNRNPA2B1 Isoform B1 of Heterogeneous nuclear	11;11;10	11;11;10	11;11;10	3	11	11	11
SOD1	SOD1	SOD1	SOD1 Superoxide dismutase [Cu-Zn];>IPI:IPI00789	4;3	4;3	4;3	2	4	4	4
IDH1	######	####	#VALUE!	6;4;3;2;2	5;3;2;2;1	5;3;2;2;1	5	6	5	5
ARID1A	ARID1A	ARID1	ARID1A Isoform 1 of AT-rich interactive domain-c	2;2;2;1;1;1;1	2;2;2;1;1;1;1	2;2;2;1;1;1;1	7	2	2	2
ARHGAP	ARHGAP	ARHG	ARHGAP17 Isoform 1 of Rho GTPase-activating pr	1;1;1;1;1;1;1;1	1;1;1;1;1;1;1;1	1;1;1;1;1;1;1;1	8	1	1	1
PPP2R4	PPP2R4	PPP2F	PPP2R4 Serine/threonine-protein phosphatase 2A r	3;3;3;3;2;2;2;2;1	3;3;3;3;2;2;2;2;1	3;3;3;3;2;2;2;2;1	14	3	3	3
FAB5	######	FABP5	FABP5;FABP5L9;FABP5L2;FABP5L7 Fatty acid-bin	4;4;1	4;4;1	4;4;1	3	4	4	4
DCK	DCK	DCK D	DCK Deoxycytidine kinase	2	2	2	1	2	2	2

FARSA	FARSA	FARS/	FARSA Phenylalanyl-tRNA synthetase alpha chain;>	2;2	2;2	2;2	2	2	2	2
BAT1	BAT1	BAT1	BAT1 Isoform 2 of Spliceosome RNA helicase BAT1	6;6;5;5;4;4;4;4;4	6;6;5;5;4;4;4;4;4	1;1;1;1;1;1;1;1;1	22	6	6	1
HNRNPH	HNRNPH	HNRN	HNRNPH3 Isoform 1 of Heterogeneous nuclear ribo	1;1;1;1;1;1;1	1;1;1;1;1;1;1	1;1;1;1;1;1;1	7	1	1	1
U2AF1	U2AF1	U2AF1	U2AF1 Splicing factor U2AF 35 kDa subunit;>IPI:I	2;2;1;1;1;1;1;1;1	2;2;1;1;1;1;1;1;1	2;2;1;1;1;1;1;1;1	9	2	2	2
SMARCC	SMARCC	SMAR	SMARCC2 Isoform 1 of SWI/SNF complex subunit !	2;2;1	2;2;1	2;2;1	3	2	2	2
NUBP1	NUBP1	NUBP	NUBP1 Isoform 1 of Cytosolic Fe-S cluster assemb	2;2	2;2	2;2	2	2	2	2
RPL14	RPL14	RPL14	RPL14 Ribosomal	2;1;1;1	2;1;1;1	2;1;1;1	4	2	2	2
BCCIP	BCCIP	BCCIF	BCCIP Isoform 2 of BRCA2 and CDKN1A-interactin	3;3;3;3;3	3;3;3;3;3	3;3;3;3;3	5	3	3	3
RAVER1	RAVER1	RAVEI	RAVER1 RAVER1	2	2	2	1	2	2	2
ILF2	ILF2	ILF2 Ir	ILF2 Interleukin enhancer-binding factor 2	11;4;3	11;4;3	11;4;3	3	11	11	11
PSMG1	PSMG1	PSMG	PSMG1 Isoform 1 of Proteasome assembly chaperc	2;2;1;1	2;2;1;1	2;2;1;1	4	2	2	2
MATR3	MATR3	MATR	MATR3 Putative uncharacterized protein MATR3;>II	2;2;1	2;2;1	2;2;1	3	2	2	2
NUCKS1	NUCKS1	NUCK	NUCKS1 Isoform 1 of Nuclear ubiquitous casein an	1;1	1;1	1;1	2	1	1	1
UBXN1	UBXN1	UBXN	UBXN1 Isoform 2 of UBX domain-containing protein	2;2;1	2;2;1	2;2;1	3	2	2	2
-	-	- 52 kI	- 52 kDa protein;>IPI:IPI00014938.3|SWISS-PROT:	4;4;3;2;2	4;4;3;2;2	4;4;3;2;2	5	4	4	4
SEPT9	SEPT9	SEPT9	SEPT9 septin 9 isoform a;>IPI:IPI00784808.1|ENSE	7;7;7;7;7;7;7;1	7;7;7;7;7;7;7;1	7;7;7;7;7;7;7;1	8	7	7	7
C1orf57	C1orf57	C1orf5	C1orf57 Chromosome 1 open reading frame 57, iso	2;2	2;2	2;2	2	2	2	2
CORO1A	CORO1A	CORC	CORO1A Coronin-1A;>IPI:IPI00642725.1|VEGA:OT	5;5;1	5;5;1	5;5;1	3	5	5	5
HPRT1	HPRT1	HPRT	HPRT1 Hypoxanthine-guanine phosphoribosyltransf	2;1	2;1	2;1	2	2	2	2
HNRNPU	HNRNPU	HNRN	HNRNPU Isoform Long of Heterogeneous nuclear ri	5;5;5;5;4	5;5;5;5;4	5;5;5;5;4	5	5	5	5
SDHA	SDHA	SDHA	SDHA cDNA FLJ61478, highly similar to Succinate	2;1	2;1	2;1	2	2	2	2
HNRNPA	HNRNPA	HNRN	HNRNPA1 Isoform A1-B of Heterogeneous nuclear	6;6;6;5;5;4;4;4;2	6;6;6;5;5;4;4;4;2	6;6;6;5;5;4;4;4;2	15	6	6	6
TUBA4A	TUBA4A	TUBA4	TUBA4A Tubulin alpha-4A chain;>IPI:IPI00794663.1	17;17;8;6;6;6;6;4	2;2;2;2;2;0;2;1;0	2;2;2;2;2;0;2;1;0	15	17	2	2
TXNL1	TXNL1	TXNL1	TXNL1 cDNA, FLJ94230, highly similar to Homo sa	5;5;1	5;5;1	5;5;1	3	5	5	5
SFRS3	SFRS3	SFRS3	SFRS3 Splicing factor, arginine/serine-rich 3;>I	3;3	2;2	2;2	2	3	2	2
NOSIP	NOSIP	NOSIF	NOSIP Nitric oxide synthase-interacting protein	1	1	1	1	1	1	1
				7;7;1	7;7;1	0;0;0	3	7	7	0
TPM3	TPM3	TPM3	TPM3 Isoform 2 of Tropomyosin alpha-3 chain;>IPI	12;12;12;11;11;1	12;12;12;11;11;1	12;12;12;11;11;1	41	12	12	12

| | | |

STIP1	STIP1	STIP1	STIP1 Stress-induced-phosphoprotein 1;>IPI:IPI00	22;18;17	22;18;17	22;18;17	3	22	22	22
C6orf108	C6orf108	C6orf1	C6orf108 Deoxyribonucleoside 5-monophosphate N	1;1	1;1	1;1	2	1	1	1
DIABLO	DIABLO	DIABL	DIABLO Diablo homolog, mitochondrial precursor;>	4;4;4;4;4;1;1	4;4;4;4;4;1;1	4;4;4;4;4;1;1	7	4	4	4
ANXA2	ANXA2	ANXA2	ANXA2 Isoform 2 of Annexin A2;>IPI:IPI00455315.4	11;11;9;9;8;4;3;	11;11;9;9;8;4;3;	11;11;9;9;8;4;3;	8	11	11	11
SNRPA	SNRPA	SNRP	SNRPA U1 small nuclear ribonucleoprotein A	3	3	2	1	3	3	2
PHGDH	PHGDH	PHGD	PHGDH D-3-phosphoglycerate dehydrogenase;>IPI	8;7	8;7	8;7	2	8	8	8
SRM	SRM	SRM S	SRM Spermidine synthase	6	6	6	1	6	6	6
TIAL1	TIAL1	TIAL1	TIAL1 TIA-1 related protein isoform 2;>IPI:IPI00	2;2;2;2;2;2;1;1;1	2;2;2;2;2;2;1;1;1	2;2;2;2;2;2;1;1;1	9	2	2	2
PPIA	PPIA	PPIA F	PPIA Peptidyl-prolyl cis-trans isomerase A;>IPI:	13;11;8;7;7;2;2;	13;11;8;7;7;2;2;	13;11;8;7;7;2;2;	18	13	13	13
NUDT1	NUDT1	NUDT	NUDT1 Isoform p26 of 7,8-dihydro-8-oxoguanine tr	2;2;2;2	2;2;2;2	2;2;2;2	4	2	2	2
NUDC	NUDC	NUDC	NUDC Nuclear migration protein nudC;>IPI:IPI0087	9;9;6;4	9;9;6;4	9;9;6;4	4	9	9	9
MDH1				8;7;6;4;2;1	8;7;6;4;2;1	8;7;6;4;2;1	6	8	8	8
CPNE1	CPNE1	CPNE	CPNE1 copine I isoform b;>IPI:IPI00018452.3|SWIS	2;2;2;2;1;1;1;1;1	2;2;2;2;1;1;1;1;1	2;2;2;2;1;1;1;1;1	13	2	2	2
CIRBP	CIRBP	CIRBF	CIRBP Cold-inducible RNA-binding protein;>IPI:IP	4;3;3;3;3;3	4;3;3;3;3;3	4;3;3;3;3;3	6	4	4	4
ATXN2L	ATXN2L	ATXN2	ATXN2L Isoform 3 of Ataxin-2-like protein;>IPI:I	3;3;3;3;3;3;3;3;3	3;3;3;3;3;3;3;3;3	3;3;3;3;3;3;3;3;3	9	3	3	3
G6PD	G6PD	G6PD	G6PD Isoform Long of Glucose-6-phosphate 1-dehy	3;3;3;3;2;2	3;3;3;3;2;2	3;3;3;3;2;2	6	3	3	3
ALDOC	ALDOC	ALDO	ALDOC Fructose-bisphos	5;4;3;2;1	4;4;2;2;1	4;4;2;2;1	5	5	4	4
PRDX2	PRDX2	PRDX	PRDX2 Peroxiredoxin-2;>IPI:IPI00909207.1|TREME	14;14;10;3	13;13;10;3	13;13;10;3	4	14	13	13
YWHAQ	YWHAQ	YWHA	YWHAQ 14-3-3 protein theta	11;5	8;4	8;4	2	11	8	8
FLNA	FLNA	FLNA	FLNA Isoform 1 of Filamin-A;>IPI:IPI00302592.2|S	8;8;8;7;3;2;2;2;2	8;8;8;7;3;2;2;2;2	8;8;8;7;3;2;2;2;2	24	8	8	8
DNAJC8	DNAJC8	DNAJ	DNAJC8 DnaJ homolog subfamily C member 8	3	3	3	1	3	3	3
				8;8;1	8;8;1	8;8;1	3	8	8	8
CNN2	CNN2	CNN2	CNN2 cDNA FLJ52765, highly similar to Calponin-2	2;2;1	2;2;1	2;2;1	3	2	2	2
BLMH	BLMH	BLMH	BLMH Bleomycin hydrolase;>IPI:IPI00794082.2|TRE	1;1	1;1	1;1	2	1	1	1
DPP3	DPP3	DPP3	DPP3 Isoform 1 of Dipeptidyl-peptidase 3	6	6	6	1	6	6	6
USP5	USP5	USP5	USP5 Isoform Long of Ubiquitin carboxyl-terminal	13;13	13;13	13;13	2	13	13	13
PAICS				19	19	2	1	19	19	2
EIF2S2	EIF2S2	EIF2S	EIF2S2 Eukaryotic translation initiation factor	3;2	3;2	3;2	2	3	3	3

TARDBP	TARDBP	TARDI	TARDBP TDP43;>IPI:IPI00639819.1|TREMBL:B1AI	4;3;2;1	4;3;2;1	4;3;2;1	4	4	4	4
TUBB4	TUBB4	TUBB4	TUBB4 Tubulin beta-4 chain;>IPI:IPI00926685.1|TR	17;16;10	2;2;1	2;2;1	3	17	2	2
PAFAH1E	PAFAH1I	PAFAI	PAFAH1B3 Platelet-activating factor acetylhydrol	2	2	2	1	2	2	2
MCM6	MCM6	MCM6	MCM6 DNA replication licensing factor MCM6	7;1	7;1	7;1	2	7	7	7
TMPO	TMPO	TMPO	TMPO Lamina-associated polypeptide 2, isoform al	7	2	2	1	7	2	2
KHSRP	KHSRP	KHSR	KHSRP KH-type splicing regulatory protein;>IPI:I	16;15;9	16;15;9	15;14;9	3	16	16	15
HNRNPH	HNRNPH	HNRN	HNRNPH1 51 kDa protein;>IPI:IPI00013881.6|SWIS	4;4;3;2	2;2;2;1	2;2;2;1	4	4	2	2
STMN1	######	####	#VALUE!	12;10;10;9;8;3;1	12;10;10;9;8;3;1	9;7;7;6;5;0;0;0;0	10	12	12	9
PTBP1	PTBP1	PTBP1	PTBP1 polypyrimidine tract-binding protein 1 iso	7;7;7;4;2;1;1;1;1	7;7;7;4;2;1;1;1;1	7;7;7;4;2;1;1;1;1	11	7	7	7
UBE2L3	UBE2L3	UBE2L	UBE2L3 Ubiquitin carrier protein;>IPI:IPI0002134	2;2;2	2;2;2	2;2;2	3	2	2	2
HDGF	HDGF	HDGF	HDGF hepatoma-derived growth factor isoform b;>I	6;6;6;3	6;6;6;3	6;6;6;3	4	6	6	6
CXorf26	CXorf26	CXorf2	CXorf26 UPF0368 protein Cxorf26	2	2	2	1	2	2	2
MTAP	MTAP	MTAP	MTAP cDNA FLJ59758, highly similar to S-methyl-5	2;2;1;1;1	2;2;1;1;1	2;2;1;1;1	5	2	2	2
CHMP4B	CHMP4B	CHMP	CHMP4B Charged multivesicular body protein 4b	2	2	2	1	2	2	2
MCM4	MCM4	MCM4	MCM4 DNA replication licensing factor MCM4;>IPI:	4;4	4;4	4;4	2	4	4	4
HNRNPC	HNRNPC	HNRN	HNRNPC Isoform C2 of Heterogeneous nuclear ribo	4;4;4;4;4;4;3;2;2	4;4;4;4;4;4;3;2;2	4;4;4;4;4;4;3;2;2	12	4	4	4
PTMA;PT	PTMA;PT	PTMA	PTMA;PTMAP5 Isoform 1 of Prothymosin alpha;>IP	5;5;5;5;4;4;4;4;4	5;5;5;5;4;4;4;4;4	5;5;5;5;4;4;4;4;4	17	5	5	5
RAD23B	RAD23B	RAD23	RAD23B UV excision repair protein RAD23 homolo	4;4;1	4;4;1	3;3;1	3	4	4	3
RAB11B	RAB11B	RAB11	RAB11B Ras-related protein Rab-11B;>IPI:IPI0042	8;7;7;7;7;2;1	8;7;7;7;7;2;1	8;7;7;7;7;2;1	7	8	8	8
IGK@,				7	1	0	1	7	1	0
SEPT7	SEPT7	SEPT7	SEPT7 Isoform 1 of Septin-7;>IPI:IPI00033025.9|E	5;5;5;4;1;1;1;1	5;5;5;4;1;1;1;1	5;5;5;4;1;1;1;1	8	5	5	5
PAICS	PAICS	PAICS	PAICS Multifunctional protein ADE2	18	1	1	1	18	1	1
ELAVL1	ELAVL1	ELAVL	ELAVL1 cDNA FLJ60076, highly similar to ELAV-lik	2;2	2;2	2;2	2	2	2	2
SAE1	SAE1	SAE1	SAE1 SUMO-activating enzyme subunit 1;>IPI:IPI0(	2;1;1	2;1;1	2;1;1	3	2	2	2
HCFC1	HCFC1	HCFC	HCFC1 Putative uncharacterized protein HCFC1;>IF	1;1;1;1	1;1;1;1	1;1;1;1	4	1	1	1
ACP1	ACP1	ACP1	ACP1 Isoform 1 of Low molecular weight phosphoty	4;3;3;2;2;2;2;1;1	4;3;3;2;2;2;2;1;1	4;3;3;2;2;2;2;1;1	10	4	4	4
ANP32E	ANP32E	ANP32	ANP32E Acidic leucine-rich nuclear phosphoprotei	3;3;2;2	3;3;2;2	3;3;2;2	4	3	3	3
SRP14	SRP14	SRP14	SRP14 Signal recognition particle 14 kDa protein	3;2;1;1;1;1	3;2;1;1;1;1	3;2;1;1;1;1	6	3	3	3

ADRM1	ADRM1	ADRM	ADRM1 Proteasomal ubiquitin receptor ADRM1;>IP	1;1	1;1	1;1	2	1	1	1
POLE3	POLE3	POLE3	POLE3 DNA polymerase epsilon subunit 3	2	2	2	1	2	2	2
PEBP1	PEBP1	PEBP1	PEBP1 Phosphatidylethanolamine-binding protein 1	11;9;7;4;1	11;9;7;4;1	11;9;7;4;1	5	11	11	11
DUT	DUT	DUT Is	DUT Isoform 1 of Deoxyuridine 5-triphosphate nuc	5;5;5;5;5	5;5;5;5;5	5;5;5;5;5	5	5	5	5
LTA4H	LTA4H	LTA4H	LTA4H Isoform 1 of Leukotriene A-4 hydrolase;>IP	3;2;2;1;1;1;1;1	3;2;2;1;1;1;1;1	3;2;2;1;1;1;1;1	8	3	3	3
CLIC4	CLIC4	CLIC4	CLIC4 Chloride intracellular channel protein 4;>	2;1	2;1	2;1	2	2	2	2
FUS	FUS	FUS F	FUS Fus-like protein (Fragment);>IPI:IPI00221354	4;4;4;4;4;4;4;2;2	4;4;4;4;4;4;4;2;2	4;4;4;4;4;4;4;2;2	9	4	4	4
hspd				6;6	6;6	6;6	2	6	6	6
UBA6	UBA6	UBA6	UBA6 Isoform 1 of Ubiquitin-like modifier-activa	2;2;2	2;2;2	2;2;2	3	2	2	2
HADHB	HADHB	HADH	HADHB Trifunctional enzyme subunit beta, mitocho	5;4;4;4;2;1	5;4;4;4;2;1	5;4;4;4;2;1	6	5	5	5
HNRNPD	HNRNPD	HNRN	HNRNPD Isoform 1 of Heterogeneous nuclear ribon	9;9;8;8;8;8	9;9;8;8;8;8	8;8;7;7;7;7	6	9	9	8
VTA1	VTA1	VTA1	VTA1 Vacuolar protein sorting-associated protein	1	1	1	1	1	1	1
NAT13	NAT13	NAT13	NAT13 Isoform 1 of N-acetyltransferase 13;>IPI:I	9;9;9;8;8;6;4;3;2	9;9;9;8;8;6;4;3;2	9;9;9;8;8;6;4;3;2	9	9	9	9
OTUB1	OTUB1	OTUB	OTUB1 cDNA FLJ56307, highly similar to Ubiquitin	6;6;3	6;6;3	6;6;3	3	6	6	6
RUVBL2	RUVBL2	RUVB	RUVBL2 RuvB-like 2;>IPI:IPI00909925.1|TREMBL:I	6;3	6;3	6;3	2	6	6	6
VAPA	VAPA	VAPA	VAPA vesicle-associated membrane protein-associa	3;3;3;2;1;1	3;3;3;2;1;1	3;3;3;2;1;1	6	3	3	3
PCBP1	PCBP1	PCBP1	PCBP1 Poly(rC)-binding protein 1	7	7	5	1	7	7	5
DRG1	DRG1	DRG1	DRG1 Developmentally-regulated GTP-binding prot	2;2	2;2	2;2	2	2	2	2
UBE2K	UBE2K	UBE2I	UBE2K Isoform 1 of Ubiquitin-conjugating enzyme	6;5;5;2	6;5;5;2	6;5;5;2	4	6	6	6
				2;2;1;1;1;1;1	2;2;1;1;1;1;1	2;2;1;1;1;1;1	7	2	2	2
SFPQ	SFPQ	SFPQ	SFPQ Isoform Long of Splicing factor, proline- a	13;12	13;12	12;11	2	13	13	12
PSMF1	PSMF1	PSMF	PSMF1 Proteasome inhibitor PI31 subunit;>IPI:IPI	2;2;2;1;1	2;2;2;1;1	2;2;2;1;1	5	2	2	2
ACTL6A	ACTL6A	ACTL6	ACTL6A Isoform 1 of Actin-like protein 6A;>IPI:I	2;2;1;1;1	2;2;1;1;1	2;2;1;1;1	5	2	2	2
ACAT1	ACAT1	ACAT1	ACAT1 Acetyl-CoA acetyltransferase, mitochondria	4;2	4;2	4;2	2	4	4	4
MAPRE1	MAPRE1	MAPR	MAPRE1 Microtubule-associated protein RP/EB fan	7;7	7;7	7;7	2	7	7	7
RAC2	RAC2	RAC2	RAC2 Ras-related C3 botulinum toxin substrate 2;	3;3;3;2	1;1;1;1	1;1;1;1	4	3	1	1
VCL	VCL	VCL Is	VCL Isoform 2 of Vinculin;>IPI:IPI00291175.7|SWI	10;10;2;2;2	10;10;2;2;2	10;10;2;2;2	5	10	10	10
PPAT	PPAT	PPAT	PPAT Amidophosphoribosyltransferase	3;1	3;1	3;1	2	3	3	3

IPO9	IPO9	IPO9 I	IPO9 Importin-9	3	3	3	1	3	3	3	
RPL8	RPL8	RPL8	RPL8 32 kDa protein;>IPI:IPI00012772.8|SWISS-PI	1;1;1;1;1	1;1;1;1;1	1;1;1;1;1	5	1	1	1	
######	######	LOC72	LOC723972;ANP32A Acidic leucine-rich nuclear ph	5;5;5;2;2;1;1	5;5;5;2;2;1;1	4;4;4;2;2;1;1	7	5	5	4	
RPS4X	RPS4X	RPS4X	RPS4X 40S ribosomal protein S4, X isoform;>IPI:I	6;3;2;2;2;2;1;1	6;3;2;2;2;2;1;1	6;3;2;2;2;2;1;1	8	6	6	6	
ARL3	ARL3	ARL3	ARL3 ADP-ribosylation factor-like protein 3	5	5	5	1	5	5	5	
C11orf54	C11orf54	C11orf	C11orf54 Isoform 1 of Ester hydrolase C11orf54;>	2;2;2;1	2;2;2;1	2;2;2;1	4	2	2	2	
				4;4;4;4;4;3;3;3;2	2;2;2;2;2;1;1;1;0	2;2;2;2;2;1;1;1;0	15	4	2	2	
ACTR1A	ACTR1A	ACTR	ACTR1A Alpha-centractin;>IPI:IPI00908883.2|TREM	4;4;1;1	4;4;1;1	4;4;1;1	4	4	4	4	
EIF3G	EIF3G	EIF3G	EIF3G Eukaryotic translation initiation factor 3	3;1	3;1	3;1	2	3	3	3	
HNRNPK	HNRNPK	HNRN	HNRNPK Isoform 2 of Heterogeneous nucle	13;13;12;12;12;(	13;13;12;12;12;(	13;13;12;12;12;(	7	13	13	13	
SNRPD2	SNRPD2	SNRP	SNRPD2 Small nuclear ribonucleoprotein Sm D2;>I	6;4;4;2	6;4;4;2	6;4;4;2	4	6	6	6	
TOMM34	TOMM34	TOMM	TOMM34 Mitochondrial import receptor subunit TOM	3;2	3;2	3;2	2	3	3	3	
SEC31A	SEC31A	SEC31	SEC31A Isoform 8 of Protein transport protein Se	2;2;2;2;2;2;2;2;1	2;2;2;2;2;2;2;2;1	2;2;2;2;2;2;2;2;1	9	2	2	2	
CDK4	CDK4	CDK4	CDK4 Cell division protein kinase 4	5;2;1	4;2;1	4;2;1	3	5	4	4	
RPS5	RPS5	RPS5	RPS5 40S ribosomal protein S5	6;2	6;2	6;2	2	6	6	6	
RPS10	RPS10	RPS10	RPS10 40S ribosomal protein S10;>IPI:IPI0074951	9;8;7;4;4;4;2	9;8;7;4;4;4;2	9;8;7;4;4;4;2	7	9	9	9	
RPL6	RPL6	RPL6	RPL6 60S ribosomal protein L6;>IPI:IPI00329389.8	2;2;2;1	2;2;2;1	2;2;2;1	4	2	2	2	
EHD1	EHD1	EHD1	EHD1 EH domain-containing protein 1;>IPI:	3;3;2;2;1;1;1	3;3;2;2;1;1;1	3;3;2;2;1;1;1	7	3	3	3	
AHSA1	AHSA1	AHSA	AHSA1 Activator of 90 kDa heat shock protein ATP	4	4	4	1	4	4	4	
NAPG	NAPG	NAPG	NAPG Gamma-soluble NSF attachment protein;>IP	2;2	2;2	2;2	2	2	2	2	
ANXA11	######	####	#VALUE!	5;5;2	5;5;2	5;5;2	3	5	5	5	
RSAP15	######	RPSA	RPSAP15;RPSA 33 kDa protein;>IPI:IPI00553164.4	9;9;9;8;8;7;7;5;5	9;9;9;8;8;7;7;5;5	9;9;9;8;8;7;7;5;5	17	9	9	9	
				12;12;12;12;12;1	12;12;12;12;12;1	12;12;12;12;12;1	11	12	12	12	
PSMC3	PSMC3	PSMC	PSMC3 26S protease regulatory subunit 6A	7	7	7	1	7	7	7	
MAGOHI	MAGOHI	MAGC	MAGOHB Protein mago nashi homolog 2;>IPI:IPI00	4;3;3;3;2;1;1	4;3;3;3;2;1;1	4;3;3;3;2;1;1	7	4	4	4	
-	-	- 29 kI	- 29 kDa protein;>IPI:IPI00549725.6|SWISS-PROT:	13;13;5;4;4;3;3;1	13;13;5;4;4;3;3;1	13;13;5;4;4;3;3;1	8	13	13	13	
######	######	####	#VALUE!	3;3;3;3;3;3;3;2;1	3;3;3;3;3;3;3;2;1	3;3;3;3;3;3;3;2;1	19	3	3	3	
EWSR1	EWSR1	EWSR	EWSR1 Ewing sarcoma breakpoint region 1 isoform	3;3;3;3;3;2;2;2;1	3;3;3;3;3;2;2;2;1	3;3;3;3;3;2;2;2;1	9	3	3	3	

MTHFD1	MTHFD1	MTHF	MTHFD1 cDNA FLJ56016, highly similar to C-1-tetr	23;23	23;23	23;23	2	23	23	23
TMPO	TMPO	TMPO	TMPO Isoform Beta of Lamina-associated polypepti	8;7;6;6;5;2;1	8;7;6;6;5;2;1	3;2;1;1;0;2;1	7	8	8	3
DNMT1	DNMT1	DNMT	DNMT1 Isoform 1 of DNA (cytosine-5)-methyltransf	3;3;1	3;3;1	3;3;1	3	3	3	3
PRKAR1A	PRKAR1	PRKA	PRKAR1A cAMP-dependent protein kinase	2	2	2	1	2	2	2
				4;4;1;1;1	4;4;1;1;1	4;4;1;1;1	5	4	4	4
EIF3M	EIF3M	EIF3M	EIF3M Eukaryotic translation initiation factor 3	3;1	3;1	3;1	2	3	3	3
GMPS	GMPS	GMPS	GMPS GMP synthase [glutamine-hydrolyzing];>IPI:I	2;1	2;1	2;1	2	2	2	2
KIAA0368	KIAA0368	KIAA0	KIAA0368 KIAA0368 protein	9;1	9;1	9;1	2	9	9	9
SF1	SF1	SF1 Is	SF1 Isoform 5 of Splicing factor 1;>IPI:IPI00386	2;2;2;2;2;2	2;2;2;2;2;2	2;2;2;2;2;2	7	2	2	2
FKBP3	FKBP3	FKBP3	FKBP3 FK506-binding protein 3	3	3	3	1	3	3	3
HADHA	HADHA	HADH	HADHA Trifunctional enzyme subunit alpha, mitoch	14;3	14;3	14;3	2	14	14	14
XPO1	XPO1	XPO1	XPO1 Exportin-1;>IPI:IPI0	7;7;1;1;1;1;1;1;1	7;7;1;1;1;1;1;1;1	7;7;1;1;1;1;1;1;1	9	7	7	7
TIMM44	TIMM44	TIMM4	TIMM44 Mitochondrial import inner membrane trans	2	2	2	1	2	2	2
PCBP2	PCBP2	PCBP2	PCBP2 poly(rC) binding protein 2 isoform a;>IPI:	6;6;6;6;6;6;6;3	4;4;4;4;4;4;4;1	4;4;4;4;4;4;4;1	19	6	4	4
TLN1	TLN1	TLN1	TLN1 Talin-1	36;5;2	36;5;2	36;5;2	3	36	36	36
CSNK2A1	CSNK2A	CSNK	CSNK2A1 CSNK2A1 protein;>IPI:IPI00744507.1|SV	3;3;2;2	3;3;2;2	3;3;2;2	4	3	3	3
MMS19	MMS19	MMS1	MMS19 cDNA FLJ55586, highly similar to MMS19-li	3;3;3;3;2;1;1;1;1	3;3;3;3;2;1;1;1;1	3;3;3;3;2;1;1;1;1	9	3	3	3
PPA1	PPA1	PPA1	PPA1 Inorganic pyrophosphatase;>IPI:IPI00643288	10;6;1	10;6;1	10;6;1	3	10	10	10
NUDT5	NUDT5	NUDT	NUDT5 Putative uncharacterized protein NUDT5;>I	7;7;6;6;4;1	7;7;6;6;4;1	7;7;6;6;4;1	6	7	7	7
WDR61	WDR61	WDR6	WDR61 WD repeat-containing protein 61;>IPI:IPI00	3;2;1	3;2;1	3;2;1	3	3	3	3
PGLS	PGLS	PGLS	PGLS 6-phosphogluconolactonase;>IPI:IPI0064384	4;2	4;2	4;2	2	4	4	4
EIF3B	EIF3B	EIF3B	EIF3B Isoform 2 of Eukaryotic translation initia	4;4;2;1	4;4;2;1	4;4;2;1	4	4	4	4
RPS19	RPS19	RPS19	RPS19 40S ribosomal protein S19	11	11	11	1	11	11	11
CPPED1	CPPED1	CPPE	CPPED1 Isoform 1 of Calcineurin-like phosphoeste	2;2;2	2;2;2	2;2;2	3	2	2	2
YWHAH	YWHAH	YWHA	YWHAH 14-3-3 protein eta	4;1;1	2;1;1	2;1;1	3	4	2	2
PRPF19	PRPF19	PRPF	PRPF19 Pre-mRNA-processing factor 19	2	2	2	1	2	2	2
GLOD4	GLOD4	GLOD	GLOD4 Uncharacterized protein C17orf25;>IPI:IPI0	2;2;2;2;2;1	2;2;2;2;2;1	2;2;2;2;2;1	6	2	2	2
GOT1	GOT1	GOT1	GOT1 Aspartate aminotransferase, cytoplasmic;>IP	11;9	11;9	11;9	2	11	11	11

RPL17	RPL17	RPL17	RPL17 60S ribosomal protein L1	2;2;1;1;1;1	2;2;1;1;1;1	2;2;1;1;1;1	7	2	2	2
OSBPL8	OSBPL8	OSBP	OSBPL8 Oxysterol-binding protein;>IPI:IPI0039473	1;1;1;1	1;1;1;1	1;1;1;1	4	1	1	1
SART3	SART3	SART3	SART3 Isoform 1 of Squamous cell carcinoma antig	2	2	2	1	2	2	2
AKR1A1	AKR1A1	AKR1A	AKR1A1 Alcohol dehydrogenase [NADP+];>IPI:IPI0	4;2	4;2	4;2	2	4	4	4
PDLIM1	PDLIM1	PDLIM	PDLIM1 PDZ and LIM domain protein 1	9	9	9	1	9	9	9
RPS3	RPS3	RPS3	RPS3 40S ribosomal protein S3;>IPI:IPI00939811.1	15;10;6;3	15;10;6;3	15;10;6;3	4	15	15	15
IQGAP2	IQGAP2	IQGAP	IQGAP2 Isoform 1 of Ras GTPase-activating-like p	9;7;7	8;6;6	8;6;6	3	9	8	8
CRYZ	CRYZ	CRYZ	CRYZ Quinone oxidoreductase;>IPI:IPI00647366.1|	2;2;2;2	2;2;2;2	2;2;2;2	4	2	2	2
LYPLA1	LYPLA1	LYPLA	LYPLA1 cDNA FLJ60607, highly similar to Acyl-pro	2;2;2;1;1	2;2;2;1;1	2;2;2;1;1	5	2	2	2
PPP2R1A	PPP2R1A	PPP2R	PPP2R1A Serine/threonine-protein phosphatase 2A	9;9;8;7;7;2	9;9;8;7;7;2	7;7;6;5;5;2	6	9	9	7
CAPNS1	CAPNS1	CAPNS	CAPNS1 Calpain small subunit 1	2	2	2	1	2	2	2
NCBP1	NCBP1	NCBP	NCBP1 Nuclear cap-binding protein subunit 1	4;1	4;1	4;1	2	4	4	4
SNRPD1	SNRPD1	SNRP	SNRPD1 Small nuclear ribonucleoprotein Sm D1;>I	2;1	2;1	2;1	2	2	2	2
SRI	SRI	SRI S	SRI Sorcin;>IPI:IPI00414264.4|TREMBL:A8MTH6;E	2;2;2;1	2;2;2;1	2;2;2;1	4	2	2	2
RPS2	RPS2	RPS2	RPS2 40S ribosomal protein S2	6;6;5;5;4;4;3;2;2	6;6;5;5;4;4;3;2;2	6;6;5;5;4;4;3;2;2	13	6	6	6
BTK	BTK	BTK T	BTK Tyrosine-protein kinase BTK;>I	2;2	2;2	2;2	2	2	2	2
ARHGDIA	ARHGDIA	ARHG	ARHGDIA 26 kDa protein;>IPI:IPI00003815.3|SWIS	8;8;7;7;6;6;3	8;8;7;7;6;6;3	8;8;7;7;6;6;3	7	8	8	8
######	######	####	#VALUE!	2	2	2	1	2	2	2
GMFB	GMFB	GMFB	GMFB Glia maturation factor, beta;>IPI:IPI005495	3;3	3;3	2;2	2	3	3	2
EIF3L	EIF3L	EIF3L	EIF3L Eukaryotic translation initiation factor 3	13;13;11;8;6;6;6	13;13;11;8;6;6;6	13;13;11;8;6;6;6	10	13	13	13
MSN	MSN	MSN M	MSN Moesin;>IPI:IPI00872814.1|TREMBL:A8MZ70	8;8;5;1;1	2;2;0;1;0	2;2;0;1;0	5	8	2	2
NAP1L1	NAP1L1	NAP1L	NAP1L1 Nucleosome assembly protein 1-like 1;>IPI	7;7;7;5;5	7;7;7;5;5	6;6;6;4;4	5	7	7	6
LOC7288	LOC7288	LOC72	LOC728825 Putative uncharacterized protein ENSP	2;2;2;2;1;1;1;1;1	2;2;2;2;1;1;1;1;1	2;2;2;2;1;1;1;1;1	13	2	2	2
######	######	####	#VALUE!	5;5;4;4;4;4;3	5;5;4;4;4;4;3	5;5;4;4;4;4;3	7	5	5	5
EIF6	EIF6	EIF6 E	EIF6 Eukaryotic translation initiation factor 6;	2;1;1	2;1;1	2;1;1	3	2	2	2
PITPNB	PITPNB	PITPN	PITPNB Phosphatidylinositol transfer protein, be	2;2;2;1;1	2;2;2;1;1	2;2;2;1;1	5	2	2	2
CAT	CAT	CAT C	CAT Catalase	9	9	9	1	9	9	9
ESD	ESD	ESD S	ESD S-formylglutathione hydrolase;>IPI:IPI006410	6;6;5	6;6;5	6;6;5	3	6	6	6

SNRNP7(	SNRNP7	SNRN	SNRNP70 Isoform 1 of U1 small nuclear ribonucleo	1;1;1	1;1;1	1;1;1	3	1	1	1
MCM7	MCM7	MCM7	MCM7 Isoform 1 of DNA replication licensing fact	11;10;4;2	11;10;4;2	11;10;4;2	4	11	11	11
RPS11	RPS11	RPS1:	RPS11 40S ribosomal protein S11;>IPI:IPI0074896	6;3	6;3	6;3	2	6	6	6
PARP1	PARP1	PARP:	PARP1 Poly [ADP-ribose] polymerase 1	7;1	7;1	7;1	2	7	7	7
HNRNPM	HNRNPM	HNRN	HNRNPM Isoform 1 of Heterogeneous nuclear ribor	2;2	2;2	2;2	2	2	2	2
SF3A1	SF3A1	SF3A1	SF3A1 Splicing factor 3 subunit 1	5;2;1;1	5;2;1;1	5;2;1;1	4	5	5	5
CHADL	CHADL	CHAD	CHADL Isoform 1 of Chondroadherin-like protein;>	1;1	1;1	1;1	2	1	1	1
ACO1	ACO1	ACO1	ACO1 Cytoplasmic aconitate hydratase;>IPI:IPI006	2;1	2;1	2;1	2	2	2	2
RPS3A	RPS3A	RPS3/	RPS3A 40S ribosomal protein S3a;>IPI:IPI0047211	6;6;4;1	6;6;4;1	6;6;4;1	4	6	6	6
-	-	- cDN/	- cDNA FLJ54776, highly similar to Cell division	4;4;4;1	4;4;4;1	2;2;2;0	4	4	4	2
CDK2	CDK2	CDK2	CDK2 Cell division protein kinase 2;>IPI:IPI0026	5;5;5;4;3;3	3;3;3;3;1;1	3;3;3;3;1;1	6	5	3	3
AHCY	AHCY	AHCY	AHCY Adenosylhomocysteinase;>IPI:IPI00935818.1	16;14	16;14	16;14	2	16	16	16
YARS	YARS	YARS	YARS Tyrosyl-tRNA synthetase, cytoplasmic	5	5	5	1	5	5	5
PFKL	PFKL	PFKL	PFKL 6-phosphofructokinase, liver type (EC 2.7.1	3;3;1	3;3;1	3;3;1	3	3	3	3
######	######	####	#VALUE!	8;7;6;4;3;3;1	7;6;5;3;2;3;1	7;6;5;3;2;3;1	7	8	7	7
NSF	NSF	NSF V	NSF Vesicle-fusing ATPase;>IPI:IPI00936987.1|TRI	7;7;3;2;1	7;7;3;2;1	7;7;3;2;1	5	7	7	7
-	-	- 27 kI	- 27 kDa protein;>IPI:IPI00792336.1|VEGA:OTTHUI	1;1;1;1;1;1	1;1;1;1;1;1	1;1;1;1;1;1	6	1	1	1
TMOD3	TMOD3	TMOD	TMOD3 Tropomodulin-3;>IPI:IPI00005089.1|SWISS	2;1;1	2;1;1	2;1;1	3	2	2	2
######	######	####	#VALUE!	10;10;9;6;4;4	8;8;7;4;3;3	4;4;3;3;0;0	6	10	8	4
ENO1	ENO1	ENO1	ENO1 Isoform alpha-enolase of Alpha-enolase;>IPI	27;18;2;2;2;2;2;2	27;18;2;2;2;2;2;2	27;18;2;2;2;2;2;2	10	27	27	27
APEX1	APEX1	APEX:	APEX1 DNA-(apurinic or apy	10;3	10;3	10;3	2	10	10	10
GANAB	GANAB	GANA	GANAB cDNA FLJ61290, highly similar to Neutral a	8;8;7;2	8;8;7;2	8;8;7;2	4	8	8	8
				12;12;4;4	9;9;3;3	8;8;2;2	4	12	9	8
XPNPEP1	XPNPEP	XPNPI	XPNPEP1 Xaa-Pro aminopeptidase 1;>IPI:IPI00607	3;3;3;2;1;1;1	3;3;3;2;1;1;1	3;3;3;2;1;1;1	7	3	3	3
PRDX5	PRDX5	PRDX	PRDX5 Isoform Mitochondrial of Peroxiredoxin-5,	9;9;8;4	9;9;8;4	9;9;8;4	4	9	9	9
				8;4;3;1	8;4;3;1	8;4;3;1	4	8	8	8
RAB6A	RAB6A	RAB6/	RAB6A Isoform 1 of Ras-related protein Rab-6A;>I	3;3;2;1;1;1;1;1;1	3;3;2;1;1;1;1;1;1	3;3;2;1;1;1;1;1;1	11	3	3	3
PRDX1	PRDX1	PRDX	PRDX1 Peroxiredoxin-1;>IPI:IPI00640741	17;15;8	17;15;8	14;12;5	3	17	17	14

UBE2M	UBE2M	UBE2I	UBE2M NEDD8-conjugating enzyme Ubc12	3	3	3	1	3	3	3	
RNASEH2	RNASEH	RNAS	RNASEH2A Ribonuclease H2 subunit A	5	5	5	1	5	5	5	
PCNA	PCNA	PCNA	PCNA Proliferatin	10	10	10	1	10	10	10	
XPO5	XPO5	XPO5	XPO5 Isoform 1 of Exportin-5;>IPI:IPI00747670.2|	8;8;5;4	8;8;5;4	8;8;5;4	4	8	8	8	
RAC1	RAC1	RAC1	RAC1 Isoform B of Ras-related C3 botulinum toxin	4;4;4;3	4;4;4;3	2;2;2;1	4	4	4	2	
NACA	NACA	NACA	NACA nascent polypeptide-associated complex alpl	5;5;4;4;1	5;5;4;4;1	5;5;4;4;1	5	5	5	5	
EEF1D	EEF1D	EEF1I	EEF1D Isoform 2 of Elongat	9;9;9;8;6;6;2;2	9;9;9;8;6;6;2;2	9;9;9;8;6;6;2;2	8	9	9	9	
CFL1	CFL1	CFL1 (	CFL1 Cofilin-1;>IPI:IPI00909841.1|TREMBL:B4E11	14;8;4	14;8;4	14;8;4	3	14	14	14	
C19orf10	C19orf10	C19orf	C19orf10 UPF0556 protein C19orf10	2	2	2	1	2	2	2	
ANXA7	ANXA7	ANXA	ANXA7 Isoform 1 of Annexin A7;>IPI:IPI00021771.1	5;5;5	5;5;5	5;5;5	3	5	5	5	
				22;20;19;15;12	6;6;3;5;5	5;5;3;5;4	5	22	6	5	
STMN2	STMN2	STMN	STMN2 Stathmin-2;>IPI:IPI00795953.1|VEGA:OTTH	4;4	1;1	1;1	2	4	1	1	
RPS12	RPS12	RPS12	RPS12 40S ribosomal protein S12;>IPI:IPI0015745(	4;2	4;2	4;2	2	4	4	4	
SET	SET	SET Is	SET Isoform 1 of Protein SET;>IPI:IPI00301311.1|	5;5;5;5;5;4;2;2;1	5;5;5;5;5;4;2;2;1	5;5;5;5;5;4;2;2;1	11	5	5	5	
				29;15;10;6;6;4;3	29;15;10;6;6;4;3	29;15;10;6;6;4;3	9	29	29	29	
SWAP70	SWAP70	SWAP	SWAP70 Switch-associated protein 70;>IPI:IPI0090	4;3	4;3	4;3	2	4	4	4	
TRAP1	TRAP1	TRAP:	TRAP1 Heat shock protein 75 kDa, mit	5;4	5;4	5;4	2	5	5	5	
GM2A	GM2A	GM2A	GM2A Ganglioside GM2 activator;>IPI:IPI00954213	3;2	3;2	3;2	2	3	3	3	
PARK7	######	####	#VALUE!	15	15	15	1	15	15	15	
UBE2N	UBE2N	UBE2I	UBE2N Ubiquitin-conjugating enzyme E2 N;>IPI:IPI	7;7;5;5;2	7;7;5;5;2	7;7;5;5;2	5	7	7	7	
RPL23A	RPL23A	RPL23	RPL23A Ribosomal protein L23a, isoform CRA_a;>I	3;3;3;3;3;2;2;1	3;3;3;3;3;2;2;1	3;3;3;3;3;2;2;1	8	3	3	3	
PRPF8	PRPF8	PRPF8	PRPF8 Pre-mRNA-processing-splicing factor 8	2	2	2	1	2	2	2	
ARHGDIB	ARHGDI	ARHG	ARHGDIB Rho GDP-dissociation inhibitor 2;>IPI:IP	6;6;5;4;1	6;6;5;4;1	6;6;5;4;1	5	6	6	6	
FEN1	FEN1	FEN1	FEN1 Flap endonuclease 1	6	6	6	1	6	6	6	
PDS5A	PDS5A	PDS5/	PDS5A Isoform 1 of Sister chromatid cohesion pro	2;2;1	2;2;1	2;2;1	3	2	2	2	
MRI1	MRI1	MRI1 I	MRI1 Isoform 1 of Methylthioribose-1-phosphate i	2;2	2;2	2;2	2	2	2	2	
RFC2	RFC2	RFC2	RFC2 Isoform 1 of Replication factor C subunit 2	1;1	1;1	1;1	2	1	1	1	
PSMD13	PSMD13	PSMD	PSMD13 HSPC027;>IPI:IPI00375380.4|TREMBL:B(	9;8	9;8	9;8	2	9	9	9	

UBE2I	UBE2I	UBE2I	UBE2I Ubiquitin carrier protein;>IPI:IPI00032957	2;2	2;2	2;2	2	2	2	2
NAPA	NAPA	NAPA	NAPA Alpha-soluble NSF attachment protein	5	5	5	1	5	5	5
PCMT1	PCMT1	PCMT	PCMT1 Isoform 1 of Protein-L-isoaspartate(D-aspa	13;11;11;9;3;3;3	13;11;11;9;3;3;3	13;11;11;9;3;3;3	9	13	13	13
DCTN2	DCTN2	DCTN	DCTN2 dynactin 2;>IPI:IPI00789792.1|TREMBL:A8I	4;4;2;1	4;4;2;1	4;4;2;1	4	4	4	4
LETM1	LETM1	LETM	LETM1 Isoform 1 of LETM1 and EF-hand domain-c	3	3	3	1	3	3	3
PSMD2	PSMD2	PSMD	PSMD2 26S proteasome non-ATPase regulatory su	9;9;7;6;3;3;2;1;1	9;9;7;6;3;3;2;1;1	9;9;7;6;3;3;2;1;1	9	9	9	9
PFN1	PFN1	PFN1	PFN1 Profilin-1	9;2	9;2	9;2	2	9	9	9
ABCE1	ABCE1	ABCE	ABCE1 ATP-binding cassette sub-family E member	6	6	6	1	6	6	6
PA2G4	PA2G4	PA2G	PA2G4 Proliferation-associated protein 2G4;>IPI:	9;9;8;3;2;1;1;1	9;9;8;3;2;1;1;1	9;9;8;3;2;1;1;1	8	9	9	9
SERBP1	SERBP1	SERBI	SERBP1 Isoform 1 of Plasminogen activator inhibi	4;4;4;4	4;4;4;4	4;4;4;4	4	4	4	4
PKM2	PKM2	PKM2	PKM2 Isoform M2 of Pyruvate kinase isozymes M1/	30;28;28;26;24;2	30;28;28;26;24;2	30;28;28;26;24;2	13	30	30	30
C1QBP	C1QBP	C1QBI	C1QBP Complement component 1 Q subcomponer	4;3;1	4;3;1	4;3;1	3	4	4	4
PFDN1	PFDN1	PFDN	PFDN1 Prefoldin subunit 1	2	2	2	1	2	2	2
PFAS	PFAS	PFAS	PFAS Phosphoribosylformylglycinamidine synthase;	2;2	2;2	2;2	2	2	2	2
LAP3	LAP3	LAP3	LAP3 Isoform 1 of Cytosol aminopeptidase;>IPI:IP	11;11;8	11;11;8	11;11;8	3	11	11	11
EIF3J	EIF3J	EIF3J	EIF3J Eukaryotic translation initiation factor 3	5;5	5;5	5;5	2	5	5	5
MRPL40	MRPL40	MRPL	MRPL40 39S ribosomal protein L40, mitochondrial;	2;2	2;2	2;2	2	2	2	2
EIF5A	EIF5A	EIF5A	EIF5A Isoform 2 of Eukaryotic translation initia	7;7;6;2;2;2;2	7;7;6;2;2;2;2	7;7;6;2;2;2;2	7	7	7	7
ANP32B	ANP32B	ANP32	ANP32B Isoform 1 of Acidic leucine-rich nuclear	4;4;2	3;3;1	3;3;1	3	4	3	3
RUVBL1	RUVBL1	RUVB	RUVBL1 Isoform 1 of RuvB-like 1;>IPI:IPI00788942	10;8;4;4;3;1	10;8;4;4;3;1	10;8;4;4;3;1	6	10	10	10
RPL31	RPL31	RPL31	RPL31 60S ribosomal protein L31;>IPI:IPI00917298	4;3;3;3;3;3;3;2;1	4;3;3;3;3;3;3;2;1	4;3;3;3;3;3;3;2;1	11	4	4	4
VCP	VCP	VCP T	VCP Transitional endoplasmic reticulum ATPase	29;5;4	29;5;4	29;5;4	3	29	29	29
GLRX3	GLRX3	GLRX	GLRX3 Glutaredoxin-3	6	6	6	1	6	6	6
NSFL1C	NSFL1C	NSFL1	NSFL1C Isoform 3 of NSFL1 cofactor p47;>IPI:IPI0	4;4;4;2	4;4;4;2	3;3;3;1	4	4	4	3
RCTPI1;T	RCTPI1;T	RCTPI	RCTPI1;TPI1 triosephosphate isomerase 1 isoform	20;20;16;15;3	20;20;16;15;3	20;20;16;15;3	5	20	20	20
PSMC1	PSMC1	PSMC	PSMC1 26S protease regulatory subunit 4;>IPI:IPI	6;4;4;1	6;4;4;1	6;4;4;1	4	6	6	6
######	######	####	#VALUE!	5;2;1	5;2;1	3;0;0	3	5	5	3
-	-	- Putat	- Putative uncharacterized protein RPL7P32 (Frag	3;3;3;3;3;2;2;2;1	3;3;3;3;3;2;2;2;1	3;3;3;3;3;2;2;2;1	10	3	3	3

SF3B1	SF3B1	SF3B1	SF3B1 Splicing factor 3B subunit 1	6	6	6	1	6	6	6
RPS20	RPS20	RPS2(	RPS20 ribosomal protein S20 isoform 1;>IPI:IPI00	4;4;3;2;2;2;1;1	4;4;3;2;2;2;1;1	4;4;3;2;2;2;1;1	8	4	4	4
NCAPD2	NCAPD2	NCAP	NCAPD2 Condensin complex subunit 1;>IPI:IPI004	2;2;1;1	2;2;1;1	2;2;1;1	4	2	2	2
RPS16	RPS16	RPS1(	RPS16 40S ribosomal protein S16;>IPI:IPI0039770	8;7;3	8;7;3	8;7;3	3	8	8	8
BZW2	BZW2	BZW2	BZW2 Basic leucine zipper and W2 domain-contain	4;4;4;2;2;2;2;2	4;4;4;2;2;2;2;2;2	3;3;3;2;1;2;2;1;2	11	4	4	3
STOML2	STOML2	STOM	STOML2 Stomatin-like protein 2;>IPI:IPI00908723.	3;3;1	3;3;1	3;3;1	3	3	3	3
GCN1L1	GCN1L1	GCN1	GCN1L1 Translational activator GCN1	48;3	48;3	48;3	2	48	48	48
RPLP0	RPLP0	RPLP(	RPLP0 60S acidic ribosomal protein P0;	8;7;7;6;5;5;5;5;4	8;7;7;6;5;5;5;5;4	8;7;7;6;5;5;5;5;4	12	8	8	8
RNASEH2	RNASEH	RNAS	RNASEH2B RNASEH2B protein	2	2	2	1	2	2	2
GPI	GPI	GPI G	GPI Glucose-6-phosphate isomerase;>IPI:IPI00027	14;14;13;4;2;1	14;14;13;4;2;1	14;14;13;4;2;1	6	14	14	14
######	######	CALM	CALM3;CALM2;CALM1 21 kDa protein;>IPI:IPI007	2;2;2;2;1;1;1	2;2;2;2;1;1;1	2;2;2;2;1;1;1	7	2	2	2
TRIM4	TRIM4	TRIM4	TRIM4 Isoform Alpha of Tripartite motif-containi	1;1;1;1	1;1;1;1	1;1;1;1	4	1	1	1
GAPDH	GAPDH	GAPD	GAPDH	14;13;13;11;10;8	14;13;13;11;10;8	14;13;13;11;10;8	10	14	14	14
MSH6	MSH6	MSH6	MSH6 Isoform GTBP-N of DNA mismatch repair pro	2;1	2;1	2;1	2	2	2	2
RPL7A	RPL7A	RPL7A	RPL7A 60S ribosomal protein L7a;>IPI:IPI0039767	2;2;2;1	2;2;2;1	2;2;2;1	4	2	2	2
RPL26	RPL26	RPL26	RPL26 Putative uncharacterized protein RPL26;>IP	4;4;4;3;3;2	4;4;4;3;3;2	4;4;4;3;3;2	6	4	4	4
EIF3A	EIF3A	EIF3A	EIF3A Eukaryotic translation initiation factor 3	22	22	22	1	22	22	22
RAB14	RAB14	RAB14	RAB14 Ras-related protein Rab-14;>IPI:IPI0064641	5;4	5;4	5;4	2	5	5	5
RPL4	RPL4	RPL4	RPL4 60S ribosomal protein L4;>IPI:IPI00795303.2	4;3;2;1;1;1;1;1;1	4;3;2;1;1;1;1;1;1	4;3;2;1;1;1;1;1;1	9	4	4	4
RPS13	RPS13	RPS13	RPS13 40S ribosomal protein S13	8	8	8	1	8	8	8
######	######	LOC64	LOC646214;PAK2 Serine/threonine-protein kinase F	4;2;2;2;2;2;2;1;1	4;2;2;2;2;2;2;1;1	4;2;2;2;2;2;2;1;1	9	4	4	4
RNASEH2	RNASEH	RNAS	RNASEH2C Isoform 1 of Ribonuclease H2 subunit (	3;3;2	3;3;2	3;3;2	3	3	3	3
RPL18A	RPL18A	RPL18	RPL18A 60S ribosomal protein L18a;>IPI:IPI00847	4;4;3;3;1	4;4;3;3;1	4;4;3;3;1	5	4	4	4
GAPVD1	GAPVD1	GAPV	GAPVD1 Isoform 6 of GTPase-activating protein an	2;2;2;2;2;2;2;1;1	2;2;2;2;2;2;2;1;1	2;2;2;2;2;2;2;1;1	11	2	2	2
TUBB2C	TUBB2C	TUBB2	TUBB2C Tubulin beta-2C chain;>IPI:IPI00930130.2	22;17;9;8;7;7;7;	22;17;9;8;7;7;7;	1;1;0;0;0;0;0;0;0	20	22	22	1
GLO1	GLO1	GLO1	GLO1 Lactoylglutathione lyase	8	8	8	1	8	8	8
SNRPD3	SNRPD3	SNRP	SNRPD3 Putative uncharacterized protein SNRPD3	2;2;2	2;2;2	2;2;2	3	2	2	2
RPL28	RPL28	RPL28	RPL28 ribosomal protein L28 isoform 3;>IPI:IPI00	4;4;4;4;4	4;4;4;4;4	4;4;4;4;4	5	4	4	4

ST13	ST13	ST13 I	ST13 Hsc70-interacting protein;>IPI:IPI00954445.	6;6;6;5;4;4;4;3;3	6;6;6;5;4;4;4;3;3	6;6;6;5;4;4;4;3;3	9	6	6	6
				12;12	12;12	6;6	2	12	12	6
HSPB1	HSPB1	HSPB	HSPB1 Heat shock protein beta-1;>IPI:IPI00909453	9;8;5	9;8;5	9;8;5	3	9	9	9
SNRPA1	SNRPA1	SNRP	SNRPA1 U2 small nuclear ribonucleoprotein A;>IPI	4;3;3;1	4;3;3;1	4;3;3;1	4	4	4	4
RPL23	RPL23	RPL23	RPL23 60S ribosomal protein L23;>IPI:IPI007	5;5;3;3;3;1	5;5;3;3;3;1	5;5;3;3;3;1	6	5	5	5
PPP2CA	PPP2CA	PPP2(	PPP2CA Serine/threonine-protein phosphatase 2A (	4;4;4	4;4;4	4;4;4	3	4	4	4
BUB3	BUB3	BUB3	BUB3 Mitotic checkpoint protein BUB3;>IPI:IPI005	2;2;2	2;2;2	2;2;2	3	2	2	2
VARS	VARS	VARS	VARS Valyl-tRNA synthetase;>IPI:IPI00893918.1|TF	9;9;5;3;3;3;2;2;2	9;9;5;3;3;3;2;2;2	9;9;5;3;3;3;2;2;2	9	9	9	9
THOP1	THOP1	THOP	THOP1 Thimet oligopeptidase	4;1	4;1	4;1	2	4	4	4
PPP1CB	PPP1CB	PPP1(	PPP1CB Serine/threonine-prote	10;6;5	3;2;2	3;2;2	3	10	3	3
AKR1B1	AKR1B1	AKR1E	AKR1B1 Aldose reductase;>IPI:IPI00556258.2|TRE	3;2;2;1;1;1	3;2;2;1;1;1	3;2;2;1;1;1	6	3	3	3
PRDX6	PRDX6	PRDX	PRDX6 Peroxiredoxin-6	12;3	12;3	12;3	2	12	12	12
HSP90AE	######			43;24;11;8;8;7;7	43;24;11;8;8;7;7	22;10;1;0;6;5;3;5	10	43	43	22
RPS25	RPS25	RPS2	RPS25 40S ribosomal protein S25;>IPI:IPI0090325	4;4;2	4;4;2	4;4;2	3	4	4	4
PSMA1	PSMA1	PSMA	PSMA1 Isoform Long of Proteasome subunit alpha	7;7;7;3;3	7;7;7;3;3	7;7;7;3;3	5	7	7	7
PPIF	PPIF	PPIF F	PPIF Peptidyl-prolyl cis-trans isomerase, mitoch	2;2;1	2;2;1	2;2;1	3	2	2	2
RPIA	RPIA	RPIA F	RPIA Ribose-5-phosphate isomerase	4	4	4	1	4	4	4
RPS8	RPS8	RPS8	RPS8 40S ribosomal protein S8;>IPI:IPI00645201.1	3;3	3;3	3;3	2	3	3	3
AP1B1	AP1B1	AP1B1	AP1B1 Isoform A of AP-1 complex subunit beta-1;>	4;4;4;4;4;4;1	4;4;4;4;4;4;1	2;2;2;2;2;2;0	7	4	4	2
XPOT	XPOT	XPOT	XPOT Exportin-T	5;1	5;1	5;1	2	5	5	5
RPS14	RPS14	RPS14	RPS14 40S ribosomal protein S14	5;1	5;1	5;1	2	5	5	5
C14orf16	C14orf16	C14orf	C14orf166 UPF0568 protein C14orf166;>IPI:IPI007	9;9	9;9	9;9	2	9	9	9
RPL19	RPL19	RPL19	RPL19 60S ribosomal protein L19;>IPI:IPI00175212	2;1	2;1	2;1	2	2	2	2
NAP1L4	NAP1L4	NAP1L	NAP1L4 Putative uncharacterized protein NAP1L4;>	4;4;3;3;2;1	3;3;2;2;1;1	3;3;2;2;1;1	6	4	3	3
MYH9	MYH9	MYH9	MYH9 Isoform 1 of Myosin-9;>IPI:IPI00395772.5|SV	8;6;1;1;1;1;1;1;1	8;6;1;1;1;1;1;1;1	8;6;1;1;1;1;1;1;1	17	8	8	8
PDCD5	PDCD5	PDCD	PDCD5 cDNA FLJ52456, moderately similar to Proc	2;2;1	2;2;1	2;2;1	3	2	2	2
######	######	####	#VALUE!	6;4;1	6;4;1	6;4;1	3	6	6	6
TCEB2	TCEB2	TCEB2	TCEB2 elongin B isoform b;>IPI:IPI00026670.3|SW	2;2;2	2;2;2	2;2;2	3	2	2	2

MYL12A	MYL12A	MYL12	MYL12A Myosin regulatory light chain MRCL3 varia	3;3;3;3;2;1;1;1;1	3;3;3;3;2;1;1;1;1	3;3;3;3;2;1;1;1;1	9	3	3	3
COMMD	COMMD3	COMM	COMMD3 COMM domain-containing protein 3;>IPI:	2;2;2;2;1	2;2;2;2;1	2;2;2;2;1	5	2	2	2
PSMD1	PSMD1	PSMD	PSMD1 Isoform 1 of 26S proteasome non-ATPase	5;5;2	5;5;2	5;5;2	3	5	5	5
PGK1	PGK1	PGK1	PGK1 Phosphoglycerate kinase 1;>IPI:IPI00916818	20;15;10;5;5;1	20;15;10;5;5;1	20;15;10;5;5;1	6	20	20	20
SARS	SARS	SARS	SARS Seryl-tRNA synthetase;>IPI:IPI00220637.5|S	3;3	3;3	3;3	2	3	3	3
YWHAE	YWHAE	YWHA	YWHAE 14-3-3 protein epsilon;>IPI:IPI00793344.1|	16;12;7;6;5;5;2	16;12;7;6;5;5;2	14;11;6;6;4;4;2	7	16	16	14
FUBP1	FUBP1	FUBP	FUBP1 cDNA FLJ53425, highly similar to Far upstr	4;4;4;4;4	3;3;3;3;3	3;3;3;3;3	5	4	3	3
FAM49B	FAM49B	FAM4	FAM49B Protein FAM49B;>IPI:IPI007892	5;4;2	5;4;2	4;3;1	3	5	5	4
HMGB2	HMGB2	HMGB	HMGB2 High mobility group protein B2	7	5	5	1	7	5	5
RPS26	RPS26	RPS2	RPS26 Ribosomal protein 26 (RPS26) pseudogene;	2;2;2;1;1;1;1;1;1	2;2;2;1;1;1;1;1;1	2;2;2;1;1;1;1;1;1	11	2	2	2
IQGAP1	IQGAP1	IQGAF	IQGAP1 Ras GTPase-activating-like pr	27;3	27;3	26;2	2	27	27	26
EIF4	######	EIF4A	EIF4A1;SNORA67 Eukaryotic init	11;7;7;7;5;4;3;3;	11;7;7;7;5;4;3;3;	9;5;5;5;4;3;2;2;2	15	11	11	9
EEF1B2	EEF1B2	EEF1E	EEF1B2 Elongation facto	5;3;2;1;1	5;3;2;1;1	5;3;2;1;1	5	5	5	5
CAD	CAD	CAD C	CAD CAD protein;>IPI:IPI00893035.1|TREMBL:Q53	2;2;1	2;2;1	2;2;1	3	2	2	2
RPL12	RPL12	RPL12	RPL12 Isoform 1 of 60S ribosomal protein L12;>IP	8;5;2	8;5;2	8;5;2	3	8	8	8
RFC4	RFC4	RFC4	RFC4 Replication factor C subunit 4;>IPI:IPI0092	5;4;4;4;4;2;2;1	5;4;4;4;4;2;2;1	5;4;4;4;4;2;2;1	9	5	5	5
				19;18;15;11;6;4	19;18;15;11;6;4	19;18;15;11;6;4	6	19	19	19
C11orf59	C11orf59	C11orf	C11orf59 RhoA activator C11orf59	1	1	1	1	1	1	1
######	######	####	#VALUE!	3;3	3;3	3;3	2	3	3	3
EIF3I	EIF3I	EIF3I I	EIF3I Eukaryotic translation initiation factor 3	5;1	5;1	5;1	2	5	5	5
TSNAX	TSNAX	TSNA	TSNAX Translin-associated protein X	3;1;1;1	3;1;1;1	3;1;1;1	4	3	3	3
RANBP1	RANBP1	RANB	RANBP1 Putative uncharacterized protein RANBP1	4;4;4;4;3;3;2;2;2	4;4;4;4;3;3;2;2;2	4;4;4;4;3;3;2;2;2	10	4	4	4
P4HB	P4HB	P4HB	P4HB Protein disulfide-isomerase;>IPI:IPI0087855	12;10;4;3	12;10;4;3	12;10;4;3	4	12	12	12
PRKDC	PRKDC	PRKD	PRKDC Isoform 1 of DNA-dependent protein kinase	19;19;19	19;19;19	19;19;19	3	19	19	19
HSP90AB	HSP90AI	HSP9(	HSP90AB2P Similar to Heat shock protein HSP 90-I	10	2	2	1	10	2	2
######	######	####	#VALUE!	13;6;3;3	11;5;2;2	10;4;2;2	4	13	11	10
CNDP2	CNDP2	CNDP	CNDP2 Isoform 1 of Cytosolic non-specific dipept	9;6;6;6;5;5;2;2;1	9;6;6;6;5;5;2;2;1	9;6;6;6;5;5;2;2;1	9	9	9	9
RAB1B	RAB1B	RAB1E	RAB1B Ras-related protein Rab-1B;>IPI:IPI008964	5;5;5	5;5;5	1;1;1	3	5	5	1

				78;78;77;77;18	78;78;77;77;18	78;78;77;77;18	5	78	78	78
FKBP4	FKBP4	FKBP4	FKBP4 FK506-binding protein 4	12	12	12	1	12	12	12
PSMD6	PSMD6	PSMD	PSMD6 Putative uncharacterized protein PSMD6;>I	4;4;4;4;2;1;1;1	4;4;4;4;2;1;1;1	4;4;4;4;2;1;1;1	8	4	4	4
SGTA	SGTA	SGTA	SGTA Small glutamine-rich tetratricopeptide repe	4;3	4;3	4;3	2	4	4	4
CCT8	CCT8	CCT8	CCT8 T-complex protein 1 subunit theta;>IPI:IPI0	26;26;11;6	26;26;11;6	26;26;11;6	4	26	26	26
######	######	####	#VALUE!	16;16;13;12;8;5;	16;16;13;12;8;5;	7;7;6;5;2;2;1;2;0	12	16	16	7
RPL11	RPL11	RPL11	RPL11 Isoform 1 of 60S ribosomal protein L11;>IP	3;2;1;1;1	3;2;1;1;1	3;2;1;1;1	5	3	3	3
CACYBP	CACYBP	CACY	CACYBP Isoform 1 of Calcyclin-binding protein;>I	11;8;8;5;3;3	11;8;8;5;3;3	11;8;8;5;3;3	6	11	11	11
RPL18	RPL18	RPL18	RPL18 60S ribosomal protein L18;>IPI:IPI00908950	4;3	4;3	4;3	2	4	4	4
DDX5	DDX5	DDX5	DDX5 Probable ATP-dependent RNA helicase DDX	4;4	4;4	3;3	2	4	4	3
EIF2B1	EIF2B1	EIF2B	EIF2B1 Translation initiation factor eIF-2B subu	3;2;2;1	3;2;2;1	3;2;2;1	4	3	3	3
PSMD12	PSMD12	PSMD	PSMD12 26S proteasome non-ATPase regulatory s	2;1	2;1	2;1	2	2	2	2
				9;9;9;9;5;4;4;4;4	9;9;9;9;5;4;4;4;4	9;9;9;9;5;4;4;4;4	13	9	9	9
DARS	DARS	DARS	DARS Aspartyl-tRNA synthetase, cytoplasmic	7;3;3;2;2;2	7;3;3;2;2;2	7;3;3;2;2;2	6	7	7	7
GNAS	GNAS	GNAS	GNAS Isoform XLas-1 of Guanine nucleotide-bindin	3;3;3;3;3;3;2;1	3;3;3;3;3;3;2;1	2;2;2;2;2;2;2;1	8	3	3	2
DAP3	DAP3	DAP3	DAP3 28S ribosomal protein S29, mitochondrial	3;3	3;3	3;3	2	3	3	3
STX7	STX7	STX7	STX7 Isoform 1 of Syntaxin-7;>IPI:IPI00552913.4|	5;5;4;1	5;5;4;1	5;5;4;1	4	5	5	5
PSME4	PSME4	PSME	PSME4 Isoform 1 of Proteasome activator complex	2;2;1	2;2;1	2;2;1	3	2	2	2
PSMC2	PSMC2	PSMC	PSMC2 26S protease regulatory subu	3;2	3;2	3;2	2	3	3	3
AIMP1	AIMP1	AIMP1	AIMP1 small inducible cytokine subfamily E, memb	3;3;3	3;3;3	3;3;3	3	3	3	3
######	######	####	#VALUE!	6;6;5;5;4;4	6;6;5;5;4;4	6;6;5;5;4;4	6	6	6	6
DLAT	DLAT	DLAT	DLAT Dihydrolipoyllysine-residue acetyltransfera	9;8;1	9;8;1	9;8;1	3	9	9	9
LDHB	LDHB	LDHB	LDHB L-lactate dehydrogenase B chain;>IPI:I	14;9;8	13;8;8	13;8;8	3	14	13	13
######	######	####	#VALUE!	7;6;6;1	7;6;6;1	7;6;6;1	4	7	7	7
EDF1	EDF1	EDF1	EDF1 Isoform 1 of Endothelial differentiation-re	3;3;3	3;3;3	3;3;3	3	3	3	3
CDC2	CDC2	CDC2	CDC2 Putative uncharacterized protein DKFZp686L	16;16;13;2;1;1;1	16;16;13;2;1;1;1	14;14;12;0;0;0;0	34	16	16	14
AASDHPI	AASDHP	AASDI	AASDHPPT L-aminoadipate-semialdehyde dehydro	2	2	2	1	2	2	2
RBBP4	RBBP4	RBBP4	RBBP4 Histone-binding protein RBBP4;>IPI:IPI0064	6;6;5;5;5;5;4;3;3	6;6;5;5;5;5;4;3;3	6;6;5;5;5;5;4;3;3	13	6	6	6

PPIL1	PPIL1	PPIL1	PPIL1 Peptidyl-prolyl cis-trans isomerase-like 1	3	3	3	1	3	3	3	
HSPA8	HSPA8	HSPA	HSPA8 Isoform 1 of Heat shock cognate 71 kDa pr	30;26;26;13;11;(	30;26;26;13;11;(	26;23;23;11;7;3;	10	30	30	26	
				11;11;1	11;11;1	11;11;1	3	11	11	11	
GDI2	GDI2	GDI2 (	GDI2 cDNA FLJ60299, highly similar to Rab GDP di	15;15;12;9;6;6;6	15;15;12;9;6;6;6	15;15;12;9;6;6;6	9	15	15	15	
EEF1A2	EEF1A2	EEF1A	EEF1A2 Elongation factor 1-alpha 2;>IPI:IPI00938	10;7;6	1;1;1	1;1;1	3	10	1	1	
HMGB1	HMGB1	HMGB	HMGB1	13;12;12;11;11;8	13;12;12;11;11;8	11;11;11;10;10;7	16	13	13	11	
SSBP1	SSBP1	SSBP:	SSBP1 Single-stranded DNA-	7;6;6;5	7;6;6;5	7;6;6;5	4	7	7	7	
PDCD6	PDCD6	PDCD	PDCD6 Programmed cell death protein 6;>IPI:IPI00	2;2;2	2;2;2	2;2;2	3	2	2	2	
CCT5	CCT5	CCT5	CCT5 T-complex protein 1 subunit epsilon;>IPI:IP	14;11;7	14;11;7	14;11;7	3	14	14	14	
SHMT2	SHMT2	SHMT	SHMT2 Serine hydroxymethyltransferase, mitochon	20;20;19;19;16;1	20;20;19;19;16;1	20;20;19;19;16;1	20	20	20	20	
RPS7	RPS7	RPS7	RPS7 40S ribosomal protein	8;6;5;5;5;2	8;6;5;5;5;2	8;6;5;5;5;2	6	8	8	8	
DPYSL2	DPYSL2	DPYSI	DPYSL2 Dihydropyrimidina	5;2;2;2;1	5;2;2;2;1	5;2;2;2;1	5	5	5	5	
RPS6	RPS6	RPS6	RPS6 40S ribosomal protein S6;>IPI:IPI00643522.1	2;2;1	2;2;1	2;2;1	3	2	2	2	
TCL1A	TCL1A	TCL1A	TCL1A T-cell leukemia/lymphoma protein 1A	2	2	2	1	2	2	2	
RPL10A	RPL10A	RPL10	RPL10A 60S ribosomal protein L10a;>IPI:IPI00413	2;1;1	2;1;1	2;1;1	3	2	2	2	
UGP2	UGP2	UGP2	UGP2 cDNA FLJ56155, highly similar to UTP--gluc	2;2;2;2	2;2;2;2	2;2;2;2	4	2	2	2	
GTF2I	GTF2I	GTF2I	GTF2I Isoform 1 of General transcription factor	8;8;8;8;8;5;2;1;1	8;8;8;8;8;5;2;1;1	8;8;8;8;8;5;2;1;1	14	8	8	8	
RAB2A	RAB2A	RAB2A	RAB2A Ras-related protein Rab-2A;>IPI:IPI001028	3;2;2;2;1;1;1;1;1	3;2;2;2;1;1;1;1;1	3;2;2;2;1;1;1;1;1	9	3	3	3	
######	######	####	#VALUE!	10;6;6;4	10;6;6;4	10;6;6;4	4	10	10	10	
TAGLN2	TAGLN2	TAGLI	TAGLN2 24 kDa protein;>IPI:IPI00550363.3|SWISS	14;14;13;3;1	14;14;13;3;1	14;14;13;3;1	5	14	14	14	
######	######	####	#VALUE!	9;1	9;1	9;1	2	9	9	9	
RPS24	RPS24	RPS2	RPS24 ribosomal protein S24 isoform d;>IPI:IPI00	2;2;2;2;2;2;2	2;2;2;2;2;2;2	2;2;2;2;2;2;2	7	2	2	2	
######	######	####	#VALUE!	3;3;1;1;1;1;1;1;1	3;3;1;1;1;1;1;1;1	1;1;0;0;0;0;1;0	16	3	3	1	
-	-	- Ig he	- Ig heavy chain V-II region SESS;>IPI:IPI003825	1;1	1;1	1;1	2	1	1	1	
RCC2	RCC2	RCC2	RCC2 Protein RCC2	4	4	4	1	4	4	4	
DDOST	DDOST	DDOS	DDOST Dolichyl-diphosphooligosaccharide--protein	4;4	4;4	4;4	2	4	4	4	
SUB1	SUB1	SUB1	SUB1 Activated RNA polymerase II transcriptional	4;2;1	4;2;1	4;2;1	3	4	4	4	
NPM1	NPM1	NPM1	NPM1 Isoform 1 of Nucleophosmin;>IPI:IPI0022074	4;4;3;1	4;4;3;1	4;4;3;1	4	4	4	4	

				2	2	2	1	2	2	2	
EIF3K	EIF3K	EIF3K	EIF3K Eukaryotic translation initiation factor 3	4	4	4	1	4	4	4	
NASP	NASP	NASP	NASP Isoform 3 of Nuclear autoantigenic sperm pr	5;5;5;5;1;1	5;5;5;5;1;1	5;5;5;5;1;1	6	5	5	5	
ERP29	ERP29	ERP2	ERP29 Endoplasmic reticulum protein ERp29	3;1;1	3;1;1	3;1;1	3	3	3	3	
POLD1	POLD1	POLD	POLD1 DNA polymerase;>IPI:IPI00002894.2|SWIS	3;3;3	3;3;3	3;3;3	3	3	3	3	
PSMA3	PSMA3	PSMA	PSMA3 Isoform 1 of Proteasome subunit alpha type	6;6	6;6	6;6	2	6	6	6	
CCT3	CCT3	CCT3	CCT3 T-complex protein 1 subunit gamma;>IPI:IPI	10;10;9;4;2;2;1	10;10;9;4;2;2;1	10;10;9;4;2;2;1	7	10	10	10	
RPL22	RPL22	RPL22	RPL22 60S ribosomal protein L22;>IPI:IPI00878392	2;2;1	2;2;1	2;2;1	3	2	2	2	
PDIA4	PDIA4	PDIA4	PDIA4 Protein disulfide-isomerase A4;>IPI:IPI008	5;3	5;3	5;3	2	5	5	5	
TBCD	TBCD	TBCD	TBCD Isoform 4 of Tubulin-specific chaperone D;>	2;2;1;1;1	2;2;1;1;1	2;2;1;1;1	5	2	2	2	
				2	2	2	1	2	2	2	
DCTN3	DCTN3	DCTN	DCTN3 Isoform 1 of Dynactin subunit 3;>IPI:IPI00	2;2;2;2;2	2;2;2;2;2	2;2;2;2;2	5	2	2	2	
PPP2R1B	PPP2R1I	PPP2F	PPP2R1B Isoform 2 of Serine/threonine-protein ph	3;3;3;3;3;3	1;1;1;1;1;1	1;1;1;1;1;1	6	3	1	1	
PTGES3	PTGES3	PTGE	PTGES3 Prostaglandin E synthase 3 (Cytosolic), i	5;5;5;5;5;3;2	5;5;5;5;5;3;2	5;5;5;5;5;3;2	7	5	5	5	
LONP1	LONP1	LONP	LONP1 Lon protease homolog, mitochondrial;>IPI:I	5;5;4	5;5;4	5;5;4	3	5	5	5	
ASPDH	ASPDH	ASPDI	ASPDH Putative L-aspartate dehydrogenase	1	1	1	1	1	1	1	
ARCN1	ARCN1	ARCN	ARCN1 Coatomer subunit delta variant 2;>IPI:IPI0	2;2;1;1	2;2;1;1	2;2;1;1	4	2	2	2	
GLUD1	GLUD1	GLUD	GLUD1 Glutamate dehydrogenase 1, mitochon	9;5;3	9;5;3	9;5;3	3	9	9	9	
RPS17	RPS17	RPS1	RPS17 40S ribosomal protein S17;>IPI:IPI0079115	5;4;3;2;1;1	5;4;3;2;1;1	5;4;3;2;1;1	6	5	5	5	
EIF4G1	EIF4G1	EIF4G	EIF4G1 EIF4G1 protein;>IPI:IPI00479262.4|SWISS	10;10;10;10;10;	10;10;10;10;10;	10;10;10;10;10;	26	10	10	10	
				37;10;10;9;1;1;1	37;10;10;9;1;1;1	37;10;10;9;1;1;1	9	37	37	37	
SAR1A	######	####	#VALUE!	6;2;2;2	6;2;2;2	6;2;2;2	4	6	6	6	
CMPK1	CMPK1	CMPK	CMPK1 UMP-CMP kinase 1 isoform a;>IPI:IPI0090	2;2;2;1;1	2;2;2;1;1	2;2;2;1;1	5	2	2	2	
MRPS27	MRPS27	MRPS	MRPS27 cDNA FLJ54536, highly similar to Mitocho	3;3;2	3;3;2	3;3;2	3	3	3	3	
CAPZB	CAPZB	CAPZI	CAPZB cDNA FLJ60094, highly similar to F-actin c	7;7;5;4;4;2	7;7;5;4;4;2	7;7;5;4;4;2	6	7	7	7	
CCT2	CCT2	CCT2	CCT2 T-complex protein 1 subunit beta	19;5	19;5	19;5	2	19	19	19	
VPS35	VPS35	VPS3	VPS35 Vacuolar protein sorting-associated protei	9;3	9;3	9;3	2	9	9	9	
CCT7	CCT7	CCT7	CCT7 T-complex protein 1 subunit eta;>IPI:IPI009	12;11;10;8;2;1	12;11;10;8;2;1	12;11;10;8;2;1	6	12	12	12	

EIF3E	EIF3E	EIF3E	EIF3E Eukaryotic translation initiation factor 3	13;6	13;6	13;6	2	13	13	13
RPL35	RPL35	RPL35	RPL35 60S ribosomal protein L35;>IPI:IPI00550247	3;3;2	3;3;2	3;3;2	3	3	3	3
EEF2	EEF2	EEF2	EEF2 Elongation factor 2;>IPI:IPI00909570.1|TREM	43;28;10	43;28;10	42;27;10	3	43	43	42
TCEA1	TCEA1	TCEA1	TCEA1 Isoform 1 of Transcription elongation fact	4;4;4;2;1	4;4;4;2;1	4;4;4;2;1	5	4	4	4
PFDN2	PFDN2	PFDN2	PFDN2 Prefoldin subunit 2	2	2	2	1	2	2	2
IDH2	IDH2	IDH2 I	IDH2 Isocitrate dehydrogenase [NADP], mitochondr	16;12	16;12	15;12	2	16	16	15
				6;1	6;1	6;1	2	6	6	6
				6;6;4;4;2	6;6;4;4;2	6;6;4;4;2	5	6	6	6
RPL27	RPL27	RPL27	RPL27 60S ribosomal protein L27;>IPI:IPI00790294	2;1;1	2;1;1	2;1;1	3	2	2	2
RPS15A	RPS15A	RPS15	RPS15A 40S ribosomal pr	6;2;1	6;2;1	6;2;1	3	6	6	6
SEC22B	SEC22B	SEC22	SEC22B Vesicle-trafficking protein SEC22b	5	5	5	1	5	5	5
HSPH1	HSPH1	HSPH	HSPH1 Isoform Alpha of Heat shock protein 105 kD	25;25;23;23;18;1	25;25;23;23;18;1	23;23;21;21;16;1	10	25	25	23
MARS	MARS	MARS	MARS Methionyl-tRNA synthetase, cytoplasmic;>IPI	14;9;3;2;1;1;1	14;9;3;2;1;1;1	14;9;3;2;1;1;1	7	14	14	14
UGGT1	UGGT1	UGGT	UGGT1 Isoform 1 of UDP-glucose:glycoprotein gluc	6;6;1	6;6;1	6;6;1	3	6	6	6
PSMA2	PSMA2	PSMA	PSMA2 Proteasome subunit alpha type-	6;3;2;1	6;3;2;1	6;3;2;1	4	6	6	6
EPRS	EPRS	EPRS	EPRS Bifunctional aminoacyl-tRNA synthetase;>IPI	21;14	21;14	21;14	2	21	21	21
HSD17B1	HSD17B1	HSD17	HSD17B12 Estradiol 17-beta-dehydrogenase 12	3;1	3;1	3;1	2	3	3	3
TWF2	TWF2	TWF2	TWF2 Twinfilin-2;>IPI:IPI00946809.1|ENSEMBL:EN	3;2;1;1	3;2;1;1	3;2;1;1	4	3	3	3
PSMD8	PSMD8	PSMD	PSMD8 proteasome 26S non-ATPase subunit 8;>IP	5;5;3	5;5;3	5;5;3	3	5	5	5
DDX1	DDX1	DDX1	DDX1 ATP-dependent RNA helicase DDX1	2	2	2	1	2	2	2
ATAD3A	ATAD3A	ATAD3	ATAD3A Isoform 1 of ATPase family AAA domain-c	3;3;2;2;1;1;1;1;1	3;3;2;2;1;1;1;1;1	3;3;2;2;1;1;1;1;1	14	3	3	3
CS	CS	CS Cit	CS Citrate synthase, mitochondrial;>IPI:IPI00793	8;7;7;3;3;3;2;2;2	8;7;7;3;3;3;2;2;2	8;7;7;3;3;3;2;2;2	9	8	8	8
EIF2S1	EIF2S1	EIF2S	EIF2S1 Eukaryotic translation initiation factor	3	3	3	1	3	3	3
GNB1	GNB1	GNB1	GNB1 Guanine nucleotide-binding protein G(I)/G(S	5;4;4;3	5;4;4;3	2;2;2;1	4	5	5	2
BTF3	BTF3	BTF3	BTF3 Isoform 1 of Transcription factor BTF3;>IPI	5;5;1	5;5;1	5;5;1	3	5	5	5
DNM2	DNM2	DNM2	DNM2 Isoform 1 of Dynamin-2;>IPI:IPI00514550.1|T	3;3;3;3;3;2;2;2;2	3;3;3;3;3;2;2;2;2	3;3;3;3;3;2;2;2;2	17	3	3	3
CBX3	CBX3	CBX3	CBX3 Chromobox protein homolog 3	4;1;1	4;1;1	4;1;1	3	4	4	4
ILK-2;CCT	ILK-2;CC	ILK-2;(	ILK-2;CCT4 T-complex protein 1 subunit delta;>IP	12;11;11	12;11;11	12;11;11	3	12	12	12

PSMD7	PSMD7	PSMD	PSMD7 26S proteasome non-ATPase regulatory su	2	2	2	1	2	2	2	
RPL9	RPL9	RPL9	RPL9 60S ribosoma	2;2;2;2;2;1	2;2;2;2;2;1	2;2;2;2;2;1	6	2	2	2	
TNPO1	TNPO1	TNPO	TNPO1 Isoform 1 of Transportin-1;>IPI:IPI0084387	7;7;5;2;1;1;1	7;7;5;2;1;1;1	7;7;5;2;1;1;1	7	7	7	7	
######	######	EIF3C	EIF3C;EIF3CL Putative uncharacterized protein EI	4;4;4;4;4;4	4;4;4;4;4;4	4;4;4;4;4;4	6	4	4	4	
PSMC5	PSMC5	PSMC	PSMC5 26S protease regulatory subunit 8;>IPI:IPI	4;4;4;1;1;1	4;4;4;1;1;1	4;4;4;1;1;1	6	4	4	4	
LDHA	LDHA	LDHA	LDHA lactate dehydrogenase A isoform 3;>IPI:IPI0	21;21;18;18;17;:	21;21;18;18;17;:	20;20;17;17;16;:	10	21	21	20	
ARFIP1	ARFIP1	ARFIP	ARFIP1 Isoform B of Arfaptin-1;>IPI:IPI00216520.	2;2;2;2	2;2;2;2	2;2;2;2	4	2	2	2	
RHOC	RHOC	RHOC	RHOC Ras homolog gene family, member C;>IPI:IP	2;2;2;2;2;2;2;2;1	2;2;2;2;2;2;2;2;1	2;2;2;2;2;2;2;2;1	12	2	2	2	
GSTP1	GSTP1	GSTP	GSTP1 Glutathione S-transferase P;>IPI:IPI007933	12;9;2	12;9;2	12;9;2	3	12	12	12	
PSMB3	PSMB3	PSMB	PSMB3 Proteasome subunit beta type-3;>IPI:IPI007	4;3;3	4;3;3	4;3;3	3	4	4	4	
APEH	APEH	APEH	APEH Putative uncharacterized protein APEH;>IPI:	5;5;4;4;3;1;1	5;5;4;4;3;1;1	5;5;4;4;3;1;1	8	5	5	5	
VPS29	VPS29	VPS2	VPS29 26 kDa protein;>IPI:IPI00184284.6|SWISS-F	2;2;2;1	2;2;2;1	2;2;2;1	4	2	2	2	
PSMA5	PSMA5	PSMA	PSMA5 Proteasome subunit alpha type-5	7	7	7	1	7	7	7	
NRAS	NRAS	NRAS	NRAS GTPase NRas;>IPI:IPI00423568.1|SWISS-P	2;2;2;1;1;1	2;2;2;1;1;1	2;2;2;1;1;1	6	2	2	2	
YBX1	YBX1	YBX1	YBX1 Nuclease-sensitive element-binding protein	4;4;3;3;2;2;1;1	4;4;3;3;2;2;1;1	1;1;1;0;0;1;0;0	8	4	4	1	
PSMD4	PSMD4	PSMD	PSMD4 Proteasome (Prosome, macropain) 26S sul	2;2;2;1;1	2;2;2;1;1	2;2;2;1;1	5	2	2	2	
PSMB2	PSMB2	PSMB	PSMB2 Proteasome subunit beta type-2;>IPI:IPI008	6;4	6;4	6;4	2	6	6	6	
PSMB4	PSMB4	PSMB	PSMB4 Proteasome subunit beta type-4	6	6	6	1	6	6	6	
PABPC1	PABPC1	PABP	PABPC1 Isoform 1 of Polyadenylate-binding protei	7;7;7;6;4;4;3;3;2	7;7;7;6;4;4;3;3;2	7;7;7;6;4;4;3;3;2	17	7	7	7	
SPTBN1	SPTBN1	SPTBI	SPTBN1 Isoform Long of Spectrin beta chain, brai	52;48;48;3;3;3	52;48;48;3;3;3	51;47;47;2;2;2	6	52	52	51	
DCTN1	DCTN1	DCTN	DCTN1 Putative uncharacterized protein DCTN1;>IF	2;2;2;2;2;2;2;2;1	2;2;2;2;2;2;2;2;1	2;2;2;2;2;2;2;2;1	9	2	2	2	
TUBA1A	TUBA1A	TUBA	TUBA1A Tubulin alpha-1A chain;>IPI:IPI00179709.4	19;16;16;15;14;:	2;2;2;2;2;2;1;1;0	1;1;1;1;1;1;0;1;0	10	19	2	1	
PSMA7	PSMA7	PSMA	PSMA7 Isoform 1 of Proteasome subunit alpha type	10;7;6;5;5;5;4;2	10;7;6;5;5;5;4;2	10;7;6;5;5;5;4;2	8	10	10	10	
				4;4	4;4	4;4	2	4	4	4	
IMMT	IMMT	IMMT	IMMT Isoform 1 of Mitochondrial inner membrane p	6;6;6;6;5;5;5;2;1	6;6;6;6;5;5;5;2;1	6;6;6;6;5;5;5;2;1	10	6	6	6	
				3;2;2;2	3;2;2;2	3;2;2;2	4	3	3	3	
CSE1L	CSE1L	CSE1L	CSE1L Isoform 1 of Exportin-2;>IPI:IPI00219994.2	21;21;16;10;7	21;21;16;10;7	21;21;16;10;7	5	21	21	21	
TCP1	TCP1	TCP1	TCP1 T-complex protein 1 subunit alpha;>IPI:IPI0	10;6	10;6	10;6	2	10	10	10	

				3	3	3	1	3	3	3	
SKP1	SKP1	SKP1	SKP1 Isoform 1 of S-phase kinase-associated prot	3;2;2	3;2;2	3;2;2	3	3	3	3	
CKAP5	CKAP5	CKAP!	CKAP5 Isoform 3 of Cytoskeleton-associated prote	2;2;2	2;2;2	2;2;2	3	2	2	2	
CCT6A	CCT6A	CCT6/	CCT6A T-complex protein 1 subunit zeta;>IPI:IPI0	10;7;2;1	10;7;2;1	10;7;2;1	4	10	10	10	
EIF1AY	EIF1AY	EIF1A	EIF1AY Eukaryotic translation initiation factor	2;2;2;2;1	2;2;2;2;1	2;2;2;2;1	5	2	2	2	
MYL6	MYL6	MYL6	MYL6 cDNA FLJ56329, highly similar to Myosin lig	3;3;3;3;3;3;2;2;2	3;3;3;3;3;3;2;2;2	3;3;3;3;3;3;2;2;2	13	3	3	3	
RPN1	RPN1	RPN1	RPN1 Dolichyl-diphosphooligosaccharide--protein	2;1	2;1	2;1	2	2	2	2	
RAB7A	RAB7A	RAB7/	RAB7A Ras-related protein Rab-7a;>IPI:IPI0094557	7;5;5;5;4;4;3;2;2	7;5;5;5;4;4;3;2;2	7;5;5;5;4;4;3;2;2	11	7	7	7	
RPL24	RPL24	RPL24	RPL24 19 kDa protein;>IPI:IPI00306332.4|SWISS-F	2;2;2;2	2;2;2;2	2;2;2;2	4	2	2	2	
######	######	####	#VALUE!	2;1	2;1	2;1	2	2	2	2	
RANP1;R	RANP1;F	RANP	RANP1;RAN 26 kDa protein;>IPI:IPI00795671.1|TR	11;11;11;10;6;4;	11;11;11;10;6;4;	11;11;11;10;6;4;	8	11	11	11	
PSMB1	PSMB1	PSMB	PSMB1 Proteasome subunit beta type-1	7;3	7;3	7;3	2	7	7	7	
				11	11	11	1	11	11	11	
TMEM33	TMEM33	TMEM	TMEM33 Transmembrane protein 33	1	1	1	1	1	1	1	
PGD	PGD	PGD 6	PGD 6-phosphogluconate dehydrogenase, decarbo	13;8;7	13;8;7	13;8;7	3	13	13	13	
PSMC4	PSMC4	PSMC	PSMC4 Isoform 1 of 26S protease regulatory subun	3;3;3	3;3;3	3;3;3	3	3	3	3	
CAND1	CAND1	CAND	CAND1 Isoform 1 of Cullin-associated NEDD8-diss	11;9;1	11;9;1	11;9;1	3	11	11	11	
LRRC59	LRRC59	LRRC!	LRRC59 Leucine-rich repeat-containing protein 59	6	6	6	1	6	6	6	
EIF4B	EIF4B	EIF4B	EIF4B cDNA FLJ54492, highly similar to Eukaryoti	2;2;2;2;1	2;2;2;2;1	2;2;2;2;1	5	2	2	2	
PDCD4	PDCD4	PDCD	PDCD4 Programmed cell death protein 4;>IPI:IPI00	6;6;6;3	6;6;6;3	6;6;6;3	4	6	6	6	
RPL15	######	####	#VALUE!	3;3;2;2;2;2;2;1;1	3;3;2;2;2;2;2;1;1	3;3;2;2;2;2;2;1;1	9	3	3	3	
IMPDH2	IMPDH2	IMPDH	IMPDH2 Inosine-5-monophosphate dehydrogenase	10;10;6;6;6;1	10;10;6;6;6;1	10;10;6;6;6;1	6	10	10	10	
RPLP2	RPLP2	RPLP2	RPLP2 60S acidic ribosomal protein P2	4	4	4	1	4	4	4	
BPNT1	BPNT1	BPNT1	BPNT1 Isoform 2 of 3(2),5-bisphosphate nucleotid	2;2;2;2	2;2;2;2	2;2;2;2	4	2	2	2	
COPB1	COPB1	COPB	COPB1 Coatomer subunit beta	4	4	4	1	4	4	4	
SH3BGRL	SH3BGR	SH3B(	SH3BGRL SH3 domain-binding glutamic acid-rich-li	5	5	5	1	5	5	5	
PNP	PNP	PNP c	PNP cDNA FLJ25678 fis, clone TST04067, highly si	10	10	10	1	10	10	10	
EIF4H	EIF4H	EIF4H	EIF4H Isoform Long of Eukaryotic translation ini	3;2	3;2	3;2	2	3	3	3	

C20orf3	C20orf3	C20orf	C20orf3 Isoform 1 of Adipocyte plasma membrane-a	3;3;3	3;3;3	3;3;3	3	3	3	3
SYNGR2	SYNGR2	SYNG	SYNGR2 SYNGR2 protein;>IPI:IPI00013946.1|SWI	2;2;2;1;1	2;2;2;1;1	2;2;2;1;1	5	2	2	2
SEC11A	SEC11A	SEC1	SEC11A Signal peptidase complex SPC-18;>IPI:IPI	2;2;2;2	2;2;2;2	2;2;2;2	4	2	2	2
RAP1B	RAP1B	RAP1	RAP1B Ras-related protein Rap-1b;>IPI:IPI000	5;5;5;5;4;3;3;3;2	5;5;5;5;4;3;3;3;2	5;5;5;5;4;3;3;3;2	9	5	5	5
COPG2	COPG2	COPG	COPG2 Coatomer subunit gamma-2;>IPI:IPI00877	2;1	2;1	1;1	2	2	2	1
######	######	DDB1;	DDB1;LOC100290337 DNA damage-binding protein	3;3;2;1	3;3;2;1	3;3;2;1	4	3	3	3
HSP90AA	HSP90AA	HSP90	HSP90AA1 Isoform 2 of Heat shock protein HSP 90	35;35;21;8;6;6	18;18;13;1;3;2	18;18;13;1;3;2	6	35	18	18
DCI	DCI	DCI Is	DCI Isoform 1 of 3,2-trans-enoyl-CoA isomerase,	2;2	2;2	2;2	2	2	2	2
PSMA6	PSMA6	PSMA	PSMA6 Proteasome subunit alpha type-6;>IPI:IPI00	6;3;1	6;3;1	6;3;1	3	6	6	6
TUFM	TUFM	TUFM	TUFM Tu translation elongation factor, mitochond	8	8	8	1	8	8	8
HINT2	HINT2	HINT2	HINT2 Histidine triad nucleotide-binding protein	3	3	3	1	3	3	3
HUWE1	HUWE1	HUWE	HUWE1 482 kDa protein;>IPI:IPI00456919.2|SWIS	3;3;3;3;3;1	3;3;3;3;3;1	3;3;3;3;3;1	6	3	3	3
ETFA	ETFA	ETFA	ETFA Electron transfer flavoprotein subunit alph	4;4;3	4;4;3	4;4;3	3	4	4	4
EIF4E	EIF4E	EIF4E	EIF4E eukaryotic translation initiation factor 4	2;2;2;2;1	2;2;2;2;1	2;2;2;2;1	5	2	2	2
EIF3F				9;9;1	9;9;1	9;9;1	3	9	9	9
ARF1	ARF1	ARF1	ARF1 ADP-ribosylation fa	6;6;4;4;3;3	6;6;4;4;3;3	3;3;1;2;2;1	6	6	6	3
CHCHD3	CHCHD3	CHCH	CHCHD3 Putative uncharacterized protein CHCHD3	2;2;2;2;2;1	2;2;2;2;2;1	2;2;2;2;2;1	6	2	2	2
TFG	TFG	TFG T	TFG Tyrosine-protein kinase receptor;>IPI:IPI002	3;3;3;3;3;3;2	3;3;3;3;3;3;2	3;3;3;3;3;3;2	7	3	3	3
NAMPT	NAMPT	NAMP	NAMPT Nicotinamide phosphoribosyltransferase;>IF	4;4;4;3;1;1;1	4;4;4;3;1;1;1	4;4;4;3;1;1;1	7	4	4	4
IDE	IDE	IDE In	IDE Insulin-degrading enzyme	3;1	3;1	3;1	2	3	3	3
COTL1	COTL1	COTL	COTL1 Coactosin-like protein	5	5	5	1	5	5	5
WARS	WARS	WARS	WARS Isoform 1 of Tryptophanyl-tRNA synthetase,	7;7;2	7;7;2	7;7;2	3	7	7	7
PSMD14	PSMD14	PSMD	PSMD14 26S proteasome non-ATPase regulatory s	2	2	2	1	2	2	2
HNRNPA	HNRNPA	HNRN	HNRNPAB Isoform 3 of Heterogeneous nuclear ribo	5;4;4;4;3	5;4;4;4;3	5;4;4;4;3	5	5	5	5
PDIA3	PDIA3	PDIA3	PDIA3 Protein disulfide-isomerase A3;>IPI:IPI008	12;6;4;1	12;6;4;1	8;4;0;1	4	12	12	8
NME2;NI	NME2;NI	NME2	NME2;NME1 Nucleoside diphosphate kinase;>IPI:IF	12;12;9;5;5;4;4;	12;12;9;5;5;4;4;	4;4;4;3;0;2;1;0	8	12	12	4
UBE2V2	UBE2V2	UBE2V	UBE2V2 Ubiquitin-conjugating enzyme E2 variant 2	5;4;3;3	5;4;3;3	2;1;1;0	4	5	5	2
PSME1	PSME1	PSME	PSME1 Proteasome activator complex subunit 1;>IF	10;9	10;9	10;9	2	10	10	10

BID	BID	BID Is	BID Isoform 2 of BH3-interacting domain death ag	2;2;2;1;1;1	2;2;2;1;1;1	2;2;2;1;1;1	6	2	2	2
LSP1	######	LOC3(	LOC390387;LSP1 cDNA FLJ34752 fis, clone NESO	1;1;1;1;1	1;1;1;1;1	1;1;1;1;1	5	1	1	1
RARS	RARS	RARS	RARS Isoform Complexed of Arginyl-tRNA syntheta	7;6	7;6	7;6	2	7	7	7
RPL35A	RPL35A	RPL3!	RPL35A 60S ribosomal protein L35a;>IPI	3;2;1;1	3;2;1;1	3;2;1;1	4	3	3	3
TIMM50	TIMM50	TIMM!	TIMM50 Isoform 2 of Mitochondrial import inner m	2;2	2;2	2;2	2	2	2	2
NME1	NME1	NME1	NME1 Isoform 2 of Nucleoside diphosphat	9;9;3	1;1;1	1;1;1	3	9	1	1
				10;9;2;2;1;1	10;9;2;2;1;1	10;9;2;2;1;1	6	10	10	10
COMMD	COMMD!	COMM	COMMD9 COMM domain-containing protein 9;>IPI:	1;1	1;1	1;1	2	1	1	1
TBCA	TBCA	TBCA	TBCA Tubulin-specific chaperone A;>IPI:IPI009096	5;3	5;3	5;3	2	5	5	5
TMED10	TMED10	TMED	TMED10 Transmembrane emp24 domain-containin	4;2	4;2	4;2	2	4	4	4
AK2	AK2	AK2 Is	AK2 Isoform 1 of Adenylate kinase 2, mitochondri	8;8;6;6;6;4	8;8;6;6;6;4	8;8;6;6;6;4	6	8	8	8
CAPZA1	CAPZA1	CAPZ/	CAPZA1 F-actin-capping protein subunit alpha-1;>	6;5	6;5	5;4	2	6	6	5
NDUFS3	NDUFS3	NDUF	NDUFS3 NADH dehydrogenase [ubiquinone] iron-s		5	5	5	1	5	5
PDCD6IP	PDCD6IF	PDCD	PDCD6IP programmed cell death 6 interacting prot	13;13;4;2;2;2;2;2	13;13;4;2;2;2;2;2	13;13;4;2;2;2;2;2	11	13	13	13
SPR	SPR	SPR S	SPR Sepiapterin reductase;>IPI:IPI00909276.1|TRE	2;2	2;2	2;2	2	2	2	2
HSP90B1	HSP90B1	HSP9(	HSP90B1 Endoplasmin;>IPI:IPI00939289.1|TREMB	21;13;5;3;2	19;13;3;3;2	19;13;3;3;2	5	21	19	19
NPEPPS	NPEPPS	NPEP	NPEPPS Puromycin-sensitive aminopeptidase	11;4;2;1	11;4;2;1	11;4;2;1	4	11	11	11
				12;9	12;9	12;9	2	12	12	12
PSMD11	PSMD11	PSMD	PSMD11 Proteasome 26S non-ATPase subunit 11 \	7;1	7;1	7;1	2	7	7	7
RPS23	RPS23	RPS2:	RPS23 40S ribosomal protein S23		1	1	1	1	1	1
PDIA6	PDIA6	PDIA6	PDIA6 Isoform 2 of Protein disulfide-isomerase A	10;10	10;10	10;10	2	10	10	10
SEC24C	SEC24C	SEC2-	SEC24C Protein transport protein Sec24		3	3	3	1	3	3
AARS	AARS	AARS	AARS cDNA FLJ61339, highly similar to Alanyl-tRN	17;17	17;17	17;17	2	17	17	17
APRT	APRT	APRT	APRT Adenine phosphoribosyltransferase;>IPI:IPI0	11;8;2	11;8;2	11;8;2	3	11	11	11
FMNL1	FMNL1	FMNL:	FMNL1 Isoform 2 of Formin-like protein 1;>IPI:IP	3;3;1;1	3;3;1;1	3;3;1;1	4	3	3	3
KPNB1	KPNB1	KPNB:	KPNB1 Importin subunit beta-1;>IPI:IPI00922792.1	16;10	16;10	16;10	2	16	16	16
MGMT	MGMT	MGMT	MGMT O-6-methylguanine-DNA methyltransferase;:	2;2	2;2	2;2	2	2	2	2
RPL30	RPL30	RPL3(	RPL30 60S ribosomal protein L30;>IPI:IPI00872940	3;3;2;2;1	3;3;2;2;1	3;3;2;2;1	5	3	3	3

NARG1	NARG1	NARG	NARG1 Isoform 1 of NMDA receptor-regulated prot	3;3;1;1;1;1;1	3;3;1;1;1;1;1	3;3;1;1;1;1;1	7	3	3	3
YJEFN3	YJEFN3	YJEFN	YJEFN3 cDNA FLJ58045, highly similar to NADH d	2;2;2;2;2	2;2;2;2;2	2;2;2;2;2	5	2	2	2
PSMD3	PSMD3	PSMD	PSMD3 26S proteasome non-ATPa	2	2	2	1	2	2	2
CTSS	CTSS	CTSS	CTSS Cathepsin S;>IPI:IPI00910216.1|TREMBL:B4	2;2	2;2	2;2	2	2	2	2
SF3B3	SF3B3	SF3B3	SF3B3 Isoform 1 of Splicing factor 3B subunit 3	2	2	2	1	2	2	2
RAD50	RAD50	RAD5(	RAD50 Isoform 2 of DNA repair protein RAD50;>IPI	2;2;2;1;1;1	2;2;2;1;1;1	2;2;2;1;1;1	6	2	2	2
HSPA5	HSPA5	HSPA!	HSPA5 HSPA5 protein	19	18	18	1	19	18	18
AIMP2	AIMP2	AIMP2	AIMP2 Aminoacyl tRNA synthetase complex-interac	3;3;3;3	3;3;3;3	3;3;3;3	4	3	3	3
SEC13	SEC13	SEC13	SEC13 cDNA FLJ56334, highly similar to SEC13-rel	2;2;2;2;2;2;1;1;1	2;2;2;2;2;2;1;1;1	2;2;2;2;2;2;1;1;1	14	2	2	2
EIF5	EIF5	EIF5 E	EIF5 Eukaryotic translation initiation factor 5	4;1	4;1	4;1	2	4	4	4
COPZ1	COPZ1	COPZ	COPZ1 Coatomer subunit zeta-1;>IPI:IPI00792696.	2;1	2;1	2;1	2	2	2	2
MRPL1	MRPL1	MRPL	MRPL1 39S ribosomal protein L1, mitochondrial	3	3	3	1	3	3	3
PICALM	PICALM	PICAL	PICALM Putative uncharacterized protein PICALM;>	2;2;2;2;2;2;1;1;1	2;2;2;2;2;2;1;1;1	2;2;2;2;2;2;1;1;1	9	2	2	2
UBAP2L	UBAP2L	UBAP2	UBAP2L Isoform 1 of Ubiquitin-associated protein	6;6;6;6;2;2	6;6;6;6;2;2	6;6;6;6;2;2	6	6	6	6
ACO2	ACO2	ACO2	ACO2 Aconitase 2, mitochondrial;>IPI:IPI00017855	14;14;10;7	14;14;10;7	14;14;10;7	4	14	14	14
GSTO1	GSTO1	GSTO	GSTO1 Glutathione S-transferase omega-1;>IPI:IPI	3;3;2	3;3;2	3;3;2	3	3	3	3
CALR	CALR	CALR	CALR Calreticulin	6;2	6;2	6;2	2	6	6	6
VDAC2	VDAC2	VDAC	VDAC2 Isoform 1 of Voltage-dependent anion-selec	7;7;7;7;7;6;4;4	7;7;7;7;7;6;4;4	7;7;7;7;7;6;4;4	10	7	7	7
TXNDC5	TXNDC5	TXND	TXNDC5 Thioredoxin domain-containing protein 5;>	2;2;2;2	2;2;2;2	2;2;2;2	4	2	2	2
UQCRFSL	UQCRFS	UQCR	UQCRFSL1 Cytochrome b-c1 complex subunit Ries	2;2	2;2	2;2	2	2	2	2
IDH3A	IDH3A	IDH3A	IDH3A Isoform 1 of Isocitrate dehydrogenase [NAD	4;4;3;3	4;4;3;3	4;4;3;3	4	4	4	4
TPT1	TPT1	TPT1	TPT1 Tumor protein, translationally-controlled 1	5;5;3;3;2;2;2;2;2	5;5;3;3;2;2;2;2;2	5;5;3;3;2;2;2;2;2	11	5	5	5
DDX6	DDX6	DDX6	DDX6 Probable ATP-dependent RNA helicase DDX	2	2	2	1	2	2	2
DYNC1H1	DYNC1H	DYNC	DYNC1H1 Cytoplasmic dynein 1 heavy chain 1	10	10	10	1	10	10	10
COPE	COPE	COPE	COPE Coatomer subunit epsilon;>IPI:IPI00399319.2	2;2;1	2;2;1	2;2;1	3	2	2	2
THOC6	THOC6	THOC	THOC6 Isoform 1 of THO complex subunit 6 homol	2;2;1	2;2;1	2;2;1	3	2	2	2
LARS	LARS	LARS	LARS Leucyl-tRNA synthetase, cytoplasmic;>IPI:IP	15;15;14;1	15;15;14;1	15;15;14;1	4	15	15	15
RTN4	RTN4	RTN4	RTN4 Isoform 1 of Reticulon-4;>IPI:IPI00478442.3	1;1;1	1;1;1	1;1;1	3	1	1	1

MRPL12	MRPL12	MRPL	MRPL12 cDNA FLJ60124, highly similar to Mitochor	2	2	2	1	2	2	2
HSPA4	HSPA4	HSPA4	HSPA4	14;3	12;3	12;3	2	14	12	12
PRPS2	PRPS2	PRPS2	PRPS2 Isoform 2 of Ribose-phosphate pyrophospho	2;2;2;2;2;1;1;1;1	2;2;2;2;2;1;1;1;1	2;2;2;2;2;1;1;1;1	11	2	2	2
PSMB5	PSMB5	PSMB5	PSMB5 Proteasome subunit beta type-5;>IPI:IPI009	2;2;1	2;2;1	2;2;1	3	2	2	2
TARS	TARS	TARS	TARS cDNA FLJ53464, highly similar to Threonyl-t	7;7;6;1;1;1	7;7;6;1;1;1	7;7;6;1;1;1	6	7	7	7
HADH	HADH	HADH	HADH Isoform 2 of Hydroxyacyl-coenzyme A dehyd	7;7;7	7;7;7	7;7;7	3	7	7	7
CRKL	CRKL	CRKL	CRKL Crk-like protein	3	3	3	1	3	3	3
DOCK2	DOCK2	DOCK	DOCK2 Isoform 1 of Dedicator of cytokinesis prot	2;2	2;2	2;2	2	2	2	2
DNAJA1	DNAJA1	DNAJ/	DNAJA1 DnaJ homolog subfamily A member 1	4	4	4	1	4	4	4
ETFB	ETFB	ETFB	ETFB Isoform 2 of Electron transfer flavoprotein	5;5	5;5	5;5	2	5	5	5
ACAA2	ACAA2	ACAA2	ACAA2 3-ketoacyl-CoA thiolase, mitochondrial;>IP	6;6	6;6	6;6	2	6	6	6
RQCD1	RQCD1	RQCD	RQCD1 Cell differentiation protein RCD1 homolog;	2;2;1	2;2;1	2;2;1	3	2	2	2
LOC1002	######	LOC10	LOC100291317 hypothetical protein XP_00234673	2;2;1;1	2;2;1;1	2;2;1;1	4	2	2	2
IPO7	IPO7	IPO7 I	IPO7 Importin-7	11	11	11	1	11	11	11
RAB5C	RAB5C	RAB5(	RAB5C Ras-related protein Rab-5C;>IPI:IPI007894	2;2;1;1;1;1;1;1;1	2;2;1;1;1;1;1;1;1	2;2;1;1;1;1;1;1;1	10	2	2	2
SSB	SSB	SSB L	SSB Lupus La protein;>IPI:IPI00916	5;5;2;2;1	5;5;2;2;1	5;5;2;2;1	5	5	5	5
SSR4	SSR4	SSR4	SSR4 Translocon-associated protein subuni	3;3;3	3;3;3	3;3;3	3	3	3	3
YWHAG	YWHAG	YWHA	YWHAG 14-3-3 protein gamma;>IPI:IPI00910779.1	12;9;2;1	9;6;0;0	9;6;0;0	4	12	9	9
ELMO1	######			2;1;1	2;1;1	2;1;1	3	2	2	2
FASN	FASN	FASN	FASN Fatty acid synthase	30	30	30	1	30	30	30
OLA1	OLA1	OLA1	OLA1 47 kDa protein;>IPI:IPI00290416.3|SWISS-PI	3;3;2;2;2;1	3;3;2;2;2;1	3;3;2;2;2;1	6	3	3	3
TKT				15;15;15;15;13;	15;15;15;15;13;	15;15;15;15;13;	8	15	15	15
PHB2	PHB2	PHB2	PHB2 Prohibitin-2;>IPI:IPI00797822.2|TREMBL:B4[	14;12	14;12	14;12	2	14	14	14
PSME2	PSME2	PSME	PSME2 Putative uncharacterized protein PSME2;>I	9;9;9;4	9;9;9;4	9;9;9;4	4	9	9	9
HSPA6	HSPA6	HSPA(	HSPA6 Heat shock 70 kDa protein 6;>IPI:IPI000111	6;3	1;1	1;1	2	6	1	1
CAPRIN1				2;2;2	2;2;2	2;2;2	3	2	2	2
G3BP1	G3BP1	G3BP:	G3BP1 Ras GTPase-activating protein-	5;2	5;2	5;2	2	5	5	5
TOMM2	TOMM22	TOMM	TOMM22 Mitochondrial import receptor subunit TOM	2	2	2	1	2	2	2

SIRT3	SIRT3	SIRT3	SIRT3 cDNA FLJ60939, highly similar to NAD-depe	3;3;2;2	3;3;2;2	3;3;2;2	4	3	3	3
HMGA1	HMGA1	HMGA	HMGA1 cDNA FLJ54188, moderately similar to Higl	2;2;2;2;2;2	2;2;2;2;2;2	2;2;2;2;2;2	6	2	2	2
PMVK	PMVK	PMVK	PMVK Phosphomevalonate kinase	3	3	3	1	3	3	3
DLSTP;DI	DLSTP;D	DLSTI	DLSTP;DLST Dihydrolipoyllysine-residue succinylt	3;3;2;2;2	3;3;2;2;2	3;3;2;2;2	5	3	3	3
HINT1	HINT1	HINT1	HINT1 Histidine triad nucleotide-binding protein	2;1	2;1	2;1	2	2	2	2
ANXA5	ANXA5	ANXA!	ANXA5 Annexin A5;>IPI:IPI00872379.1|TREMBL:A	17;17	17;17	17;17	2	17	17	17
SLC25A3	SLC25A3	SLC25	SLC25A3 Isoform A of Phosphate carrier protein,	2;2;2;2;2;1	2;2;2;2;2;1	2;2;2;2;2;1	6	2	2	2
GLS	GLS	GLS Is	GLS Isoform KGA of Glutaminase kidney isoform, m	2;2;1;1	2;2;1;1	2;2;1;1	4	2	2	2
VDAC3	VDAC3	VDAC	VDAC3 Isoform 2 of Voltage-dependent anion-selec	3;3	3;3	3;3	2	3	3	3
APOO	APOO	APOO	APOO Isoform 1 of Apolipoprotein O;>IPI:IPI00797	2;2;2;2	2;2;2;2	2;2;2;2	4	2	2	2
QSOX1	QSOX1	QSOX	QSOX1 Isoform 1 of Sulfhydryl oxidase 1;>IPI:IPI	1;1	1;1	1;1	2	1	1	1
PDHB	PDHB	PDHB	PDHB Isoform 1 of Pyruvate dehydrogenase E1 con	5;5;5;5;3;3;2	5;5;5;5;3;3;2	5;5;5;5;3;3;2	7	5	5	5
TMEM10	TMEM10	TMEM	TMEM109 Transmembrane protein 109;>IPI:IPI009	1;1	1;1	1;1	2	1	1	1
KARS	KARS	KARS	KARS Isoform Cytoplasmic of Lysyl-tRNA synthetas	5;3;3	5;3;3	5;3;3	3	5	5	5
PRDX3	PRDX3	PRDX	PRDX3 Thioredoxin-dependent peroxide reductase,	10;10	10;10	10;10	2	10	10	10
SSR1	SSR1	SSR1	SSR1 Putative uncharacterized protein SSR1;>IPI:	1;1;1;1;1	1;1;1;1;1	1;1;1;1;1	5	1	1	1
LOC7295	LOC729	LOC7	LOC729595 similar to high mobility group box 3;>	2;2;2;2;2;2;2;1;1	2;2;2;2;2;2;2;1;1	2;2;2;2;2;2;2;1;1	12	2	2	2
FIS1	FIS1	FIS1 M	FIS1 Mitochondrial fission 1 protein	2	2	2	1	2	2	2
UQCRC2	UQCRC2	UQCR	UQCRC2 Cytochrome b-c1 complex subunit 2, mito	5	5	5	1	5	5	5
ATP5C1	ATP5C1	ATP5(	ATP5C1 Isoform Liver of ATP synthase subunit gam	4;3	4;3	4;3	2	4	4	4
PSMB8	PSMB8	PSMB	PSMB8 Isoform 1 of Proteasome subunit beta type-	3;3;3;2;2;1	3;3;3;2;2;1	3;3;3;2;2;1	6	3	3	3
PHB	PHB	PHB P	PHB Prohibitin;>IPI:IPI00793658.1|TREM	16;11;11;9;7;1;1	16;11;11;9;7;1;1	16;11;11;9;7;1;1	7	16	16	16
C14orf15	C14orf15	C14orf	C14orf156 SRA stem-loop-interacting RNA-binding	2	2	2	1	2	2	2
LCP1	LCP1	LCP1	LCP1 Plastin-2	43;12;11;8;8;3;3	43;12;11;8;8;3;3	43;12;11;8;8;3;3	10	43	43	43
HCLS1	HCLS1	HCLS:	HCLS1 Hematopoietic lineage cell-specific protei	3;3	3;3	3;3	2	3	3	3
ATP5A1	ATP5A1	ATP5A	ATP5A1 ATP synthase subunit alpha, mitochondrial	18;15;9;8;6	18;15;9;8;6	18;15;9;8;6	5	18	18	18
SORD	SORD	SORD	SORD Sorbitol dehydrogenase;>IPI:IPI00922510.1|	2;2	2;2	2;2	2	2	2	2
CAPZA2	CAPZA2	CAPZA	CAPZA2 F-actin-capping protein subunit alpha-2;>	3;2;2;2;2;1	2;1;1;1;1;1	2;1;1;1;1;1	6	3	2	2

ATP5B	ATP5B	ATP5E	ATP5B ATP synthase subunit beta, mitochondrial	22;7;4;3;3;3	22;7;4;3;3;3	22;7;4;3;3;3	6	22	22	22
PRDX4	PRDX4	PRDX	PRDX4 Peroxiredoxin-4;>IPI:IPI00647280.2|TREME	5;5;5;4	3;3;3;2	3;3;3;2	4	5	3	3
DDX3X	DDX3X	DDX3	DDX3X ATP-dependent RNA helicase DDX3X;>IPI:	3;2;2;1	3;2;2;1	3;2;2;1	4	3	3	3
MTCH2	MTCH2	MTCH	MTCH2 Mitochondrial carrier homolog 2	4	4	4	1	4	4	4
TFRC	TFRC	TFRC	TFRC Transf	6;5;1	6;5;1	6;5;1	3	6	6	6
HSD17B4	HSD17B4	HSD1	HSD17B4 Peroxisomal multifunctional enzyme type	5;2;1	5;2;1	5;2;1	3	5	5	5
UQCRC1	UQCRC1	UQCR	UQCRC1 Cytochrome b-c1 complex subunit 1, mito	3;2	3;2	3;2	2	3	3	3
HSPA9	HSPA9	HSPA	HSPA9 Stress-70 protein, mitochondrial;>IPI:IPI0	16;10	16;10	16;10	2	16	16	16
EEF1E1	EEF1E1	EEF1E	EEF1E1 Eukaryotic translation elongation factor	5;5	5;5	5;5	2	5	5	5
PTPRC	PTPRC	PTPR	PTPRC Protein tyrosine phosphatase, receptor typ	3;3;3;3;3;3	3;3;3;3;3;3	3;3;3;3;3;3	6	3	3	3
MAT2B	MAT2B	MAT2	MAT2B Isoform 1 of Methionine adenosyltransferas	2;2;2;2;1;1;1	2;2;2;2;1;1;1	2;2;2;2;1;1;1	7	2	2	2
DBNL	DBNL	DBNL	DBNL Isoform 1 of Drebrin-like protein;>IPI:IPI0	3;2;2;2;2;1;1;1;1	3;2;2;2;2;1;1;1;1	3;2;2;2;2;1;1;1;1	13	3	3	3
DAZAP1	DAZAP1	DAZAI	DAZAP1 Isoform 1 of DAZ-associated protein 1;>IP	3;3	3;3	3;3	2	3	3	3
HLA-B	HLA-B	HLA-B	HLA-B HLA class I histocompatibility antigen, B-	4;4;4;4;4;4;4;4;4	2;2;2;2;2;2;2;2;2	0;0;0;0;0;0;0;0;0	388	4	2	0
DLD	DLD	DLD D	DLD Dihydrolipoyl dehydrogenase, mit	5;5;4	5;5;4	5;5;4	3	5	5	5
PTPN1	PTPN1	PTPN	PTPN1 Tyrosine-protein phosphatase non-receptor	2	2	2	1	2	2	2
ATP5F1	ATP5F1	ATP5F	ATP5F1 ATP synthase subunit b, mitochondrial;>IP	8;6;2	8;6;2	8;6;2	3	8	8	8
TOMM70	TOMM70	TOMM	TOMM70A Mitochondrial import receptor subunit TC	2;1;1	2;1;1	2;1;1	3	2	2	2
CYB5B	CYB5B	CYB5E	CYB5B cytochrome b5 outer mitochondrial membra	3;3	3;3	3;3	2	3	3	3
MDH2	MDH2	MDH2	MDH2 Malate dehydrogenase, mitochondrial;>IPI:IP	16;13;12	16;13;12	16;13;12	3	16	16	16
ACTR2	ACTR2	ACTR	ACTR2 actin-related protein 2 isoform a;>IPI:IPI	4;4;3	4;4;3	4;4;3	3	4	4	4
SERPINB	SERPINE	SERPI	SERPINB1 Leukocyte elastase inhibitor	3	2	2	1	3	2	2
ATP5O	ATP5O	ATP5(	ATP5O ATP synthase subunit O, mitochondrial	8;3;2;2	8;3;2;2	8;3;2;2	4	8	8	8
KPNA2	KPNA2	KPNA	KPNA2 Importin subunit alpha-2;>IPI:IPI00789457.	5;5	5;5	5;5	2	5	5	5
CARS	CARS	CARS	CARS cysteinyl-tRNA synthetase isoform c;>IPI:IP	2;2;2;2;2	2;2;2;2;2	2;2;2;2;2	5	2	2	2
ATP5H	ATP5H	ATP5H	ATP5H Isoform 1 of ATP synthase subunit d, mitoc	5;5;4;1;1	5;5;4;1;1	5;5;4;1;1	5	5	5	5
SERPINB9	SERPINE	SERPI	SERPINB9 Serpin B9	4;1;1;1;1;1;1;1	4;1;1;1;1;1;1;1	3;0;0;0;0;0;0;0	8	4	4	3
UBB	######	UBB;U	UBB;UBC;RPS27A ubiquitin C;>IPI:IPI00792712.1|	2;2;2;2;2;2;2;2;2;2	2;2;2;2;2;2;2;2;2;2	2;2;2;2;2;2;2;2;2;2	23	2	2	2

RPL27A	RPL27A	RPL27	RPL27A 60S ribosomal protein L27a	1	1	1	1	1	1	1	1
HIST1H4	######	####	#VALUE!	6	6	6	1	6	6	6	6
hla-A				4;3;3;3;3;3;3;3;3	4;3;3;3;3;3;3;3;3	0;0;0;0;0;0;0;0;0	15	4	4	0	
HIST2H2	######	HIST2	HIST2H2AA4;HIST2H2AA3 Histone H2A type 2-A;>	3;3;3;3;3;3;3;2;2	3;3;3;3;3;3;3;2;2	1;1;1;1;1;1;1;1;1	9	3	3	1	
HMGN2	HMGN2	HMGN	HMGN2 Non-histone chromosomal protein HMG-17	2;1;1;1;1;1;1;1;1	2;1;1;1;1;1;1;1;1	2;1;1;1;1;1;1;1;1	10	2	2	2	
FH	FH	FH Iso	FH Isoform Mitochondrial of Fumarate hydratase,	8;8	8;8	8;8	2	8	8	8	
CANX	CANX	CANX	CANX cDNA FLJ55574, highly similar to Calnexin;>	10;10;4;3;3	10;10;4;3;3	10;10;4;3;3	5	10	10	10	
SLC3A2	######	SLC3A	SLC3A2;LOC442497 Isoform 4 of 4F2 cell-surface a	7;7;7;7;7;7;1	7;7;7;7;7;7;1	7;7;7;7;7;7;1	7	7	7	7	
ARPC3	ARPC3	ARPC	ARPC3 Actin-related protein 2/3 complex subunit	7;7;6;4;2;1	7;7;6;4;2;1	7;7;6;4;2;1	6	7	7	7	
ATP5D	ATP5D	ATP5[	ATP5D ATP synthase subunit delta, mitochondrial	2	2	2	1	2	2	2	
ATP6V1E	ATP6V1E	ATP6\	ATP6V1B2 V-type proton ATPase subunit B, brain i	2;1;1;1;1	2;1;1;1;1	2;1;1;1;1	5	2	2	2	
HARS	HARS	HARS	HARS Histidyl-tRNA synthetase, cytoplasmic;>IPI:	4;4;2;2;2;2;2;2;2	4;4;2;2;2;2;2;2;2	4;4;2;2;2;2;2;2;2	10	4	4	4	
ACLY	ACLY	ACLY	ACLY cDNA FLJ56442, highly similar to ATP-citrat	6;6;6;4	6;6;6;4	6;6;6;4	4	6	6	6	
MRE11A	MRE11A	MRE1	MRE11A cDNA FLJ38069 fis, clone CTONG2015433	3;3;3	3;3;3	3;3;3	3	3	3	3	
BRI3BP	BRI3BP	BRI3B	BRI3BP BRI3-binding protein;>IPI:IPI00152007.1|S	2;1	2;1	2;1	2	2	2	2	
hspd1				42;35;18;15;14;8	42;35;18;15;14;8	42;35;18;15;14;8	11	42	42	42	
VDAC1	VDAC1	VDAC	VDAC1 Voltage-dependent ani	13;9;7;7	13;9;7;7	13;9;7;7	4	13	13	13	
PSME3	PSME3	PSME	PSME3 Isoform 2 of Proteasome activator complex	3;3;1;1	3;3;1;1	3;3;1;1	4	3	3	3	
PPP1CA	PPP1CA	PPP1(	PPP1CA Serine/threonine-protein phosphatase PP1	11;10;8;8	11;10;8;8	4;3;1;2	4	11	11	4	
MGC295	MGC295	MGC2	MGC29506 Isoform 1 of Proapoptotic caspase adap	5;2;2	5;2;2	5;2;2	3	5	5	5	
CYCS	CYCS	CYCS	CYCS Cyt	6;6;3;2;1	6;6;3;2;1	6;6;3;2;1	5	6	6	6	
HSD17B1	HSD17B	HSD1	HSD17B10 Isoform 1 of 3-hydroxyacyl-CoA dehydro	6;5;3	6;5;3	6;5;3	3	6	6	6	
HIST2H3	######	HIST2	HIST2H3D;HIST2H3A;HIST2H3C Histone	4;4;4;4;4;4;4;3;3	4;4;4;4;4;4;4;3;3	4;4;4;4;4;4;4;3;3	14	4	4	4	
AP1G1	AP1G1	AP1G	AP1G1 cDNA FLJ46199 fis, clone TESTI4007965, h	2;2;2;2;1	2;2;2;2;1	2;2;2;2;1	5	2	2	2	
POTEE	POTEE	POTE	POTEE Isoform 1 of POTE ankyrin domain family m	8;6;6;6;6;4;2;2;2	1;1;1;1;1;1;1;1;1	0;0;0;0;0;0;0;0;0	12	8	1	0	
MT-ATP6				1	1	1	1	1	1	1	
COX4I1	COX4I1	COX4	COX4I1 Cytochrome c oxidase subunit 4 isoform 1,	4;2	4;2	4;2	2	4	4	4	
HLA-DPA	######	####	#VALUE!	2;2;2;2;1;1	2;2;2;2;1;1	2;2;2;2;1;1	6	2	2	2	
HLA-DRB1				3;3;3	3;3;3	3;3;3	3	3	3	3	

ACTN4	ACTN4	ACTN4	ACTN4 Alpha-actinin-4;>IPI:IPI00908458.1|TREMBL	37;19;18;15;14;:	37;19;18;15;14;:	37;19;18;15;14;:	19	37	37	37
MAPK1	MAPK1	MAPK1	MAPK1 Mitogen-activated protein kinase	2;2	2;2	2;2	2	2	2	2
CD74	CD74	CD74	CD74 Isoform 1 of HLA class II histocompatibilit	6;6;3	6;6;3	6;6;3	3	6	6	6
LMP2	######	####	#VALUE!	3;3;3;3;1;1	3;3;3;3;1;1	3;3;3;3;1;1	6	3	3	3
SFXN1	SFXN1	SFXN1	SFXN1 Sideroflexin-1	4	4	4	1	4	4	4
HLA-DRB5				8;6;6;4;3;3;3;3;3	8;6;6;4;3;3;3;3;3	4;4;3;0;0;0;0;0;0	21	8	8	4
hla-dra	######	####	#VALUE!	5;5;5;5;3;2;2;2;1	5;5;5;5;3;2;2;2;1	4;4;4;4;2;2;2;2;0	16	5	5	4
GOT2	GOT2	GOT2	GOT2 Aspartate aminotransferase, mitochondrial;>	10;9	10;9	10;9	2	10	10	10
PYCR2	PYCR2	PYCR2	PYCR2 Pyrroline-5-carboxylate reductase 2;>IPI:I	1;1	1;1	1;1	2	1	1	1
HLA-DPB1				4;4;4;3;2;2;2;2;2	4;4;4;3;2;2;2;2;2	3;3;3;2;1;1;1;1;1	13	4	4	3
SLC25A5	SLC25A5	SLC25	SLC25A5 ADP/ATP translocase 2	10	10	4	1	10	10	4
NDUFAF2	NDUFAF	NDUF	NDUFAF2 Mimitin, mitochondrial	2	2	2	1	2	2	2
HIST2H2I	HIST2H2	HIST2	HIST2H2BF Histone H2B;>IPI:IPI00794461.1|SWIS	6;6;6;6;6;6;6;6;6	6;6;6;6;6;6;6;6;6	6;6;6;6;6;6;6;6;6	22	6	6	6
EBP	EBP	EBP 3	EBP 3-beta-hydroxysteroid-Delta(8),Delta(7)-isom	2;1;1	2;1;1	2;1;1	3	2	2	2
ACTR3	ACTR3	ACTR3	ACTR3 Actin-related protein 3	6;1;1;1;1;1;1	6;1;1;1;1;1;1	6;1;1;1;1;1;1	7	6	6	6
ARPC4	TTLL3;AI	TTLL3	TTLL3;ARPC4 Putative uncharacterized protein ARI	5;5;5;4;4;4;3;2;1	5;5;5;4;4;4;3;2;1	5;5;5;4;4;4;3;2;1	10	5	5	5
ECH1	ECH1	ECH1	ECH1 Delta(3,5)-Delta(2,4)-dienoyl-CoA isomerase	1	1	1	1	1	1	1
MT-CO2	######	####	#VALUE!	4	4	4	1	4	4	4
LOC646048				1;1	1;1	1;1	2	1	1	1
ARPC2	ARPC2	ARPC2	ARPC2 Actin-related protein 2/3 complex subunit	4;2;2;2;2;1	4;2;2;2;2;1	4;2;2;2;2;1	6	4	4	4
ACTG1	ACTG1	ACTG1	ACTG1 Actin, cytoplasmic 2;>IPI:IPI00930226.1|TR	21;21;9;9	1;1;1;1	1;1;1;1	4	21	1	1
HLA-DRB	######	LOC10	LOC100133811;HLA-DRB1;LOC100294468;LOC10	5	2	0	1	5	2	0
ACTBL2	ACTBL2	ACTBL2	ACTBL2 Beta-actin-like protein 2	6;1	1;0	1;0	2	6	1	1
MS4A1	MS4A1	MS4A1	MS4A1 B-lymphocyte antigen CD20;>IPI:IPI009105	4;2	4;2	4;2	2	4	4	4
CLTC	CLTC	CLTC	CLTC Isoform 1 of Clathrin heavy chain 1;>IPI:IP	26;26;7;7	26;26;7;7	26;26;7;7	4	26	26	26
ACTA1	ACTA1	ACTA1	ACTA1 Actin, alpha skeletal muscle;>IPI:IPI00023	12;12;12;11;11;:	1;1;1;1;1;1;1;1;1	1;1;1;1;1;1;1;1;1	14	12	1	1
FDFT1	FDFT1	FDFT1	FDFT1 Squalene synthetase;>IPI:IPI00	3;2;2	3;2;2	3;2;2	3	3	3	3
HLA-DPB	-	- cDN	- cDNA FLJ75434, highly similar to Homo sapiens	3;3;3;3;3;2;2;1	2;2;2;2;2;1;1;1	2;2;2;2;2;1;1;1	8	3	2	2

PLCG2	PLCG2	PLCG:	PLCG2 1-phosphatidylinositol-4,5-bisphosphate ph	7	7	7	1	7	7	7
HMGCS1	HMGCS1	HMGC	HMGCS1 Hydroxymethylglutaryl-CoA synthase, cyto	6;1;1	6;1;1	6;1;1	3	6	6	6
SLC25A6	SLC25A6	SLC25	SLC25A6 ADP/ATP translocase 3;>IPI:IPI00645646	10;7	4;2	3;2	2	10	4	3
ATP6V1E	ATP6V1E	ATP6\	ATP6V1E1 V-type proton ATPase subunit E 1;>IPI:I	1;1;1	1;1;1	1;1;1	3	1	1	1
IPO5				9;9;7;3;3;3;3;3	9;9;7;3;3;3;3;3	9;9;7;3;3;3;3;3	18	9	9	9
PPP1CC	PPP1CC	PPP1(	PPP1CC Isoform Gamma-2 of Serine/threonine-pro	9;9;6;6;1	2;2;0;0;0	2;2;0;0;0	5	9	2	2
HLA-DQ	-	- HLA	- HLA class II histocompatibility antigen, DQ(1)	3;3;3;3;3;2;2;1	2;2;2;2;2;2;1;1;1	2;2;2;2;2;2;1;1;1	11	3	2	2
SOD2	SOD2	SOD2	SOD2 Superoxide dismutase [Mn], mitochondrial;>I	2;2;2;1	2;2;2;1	2;2;2;1	4	2	2	2
Gab1	GAB1	GAB1	GAB1 Isoform 2 of GRB2-associated-binding protei	2;2	2;2	2;2	2	2	2	2
LNPEP	LNPEP	LNPEI	LNPEP Isoform 1 of Leucyl-cystinyl aminopeptidas	2;2;2;2	2;2;2;2	2;2;2;2	4	2	2	2
LYN	LYN	LYN L	LYN LYN protein (Fragment);>IPI:IPI00432416.4|SV	4;4;3;3;1;1;1;1;1	4;4;3;3;1;1;1;1;1	4;4;3;3;1;1;1;1;1	14	4	4	4
LMNB2	LMNB2	LMNB	LMNB2 Lamin-B2;>IPI:IPI00879819.1|SWISS-PRO	10;10;1;1;1;1;1;1	8;8;0;0;0;0;0;0;0	8;8;0;0;0;0;0;0;0	11	10	8	8
INPP5D	######	INPP5	INPP5D;LOC646743 Isoform 1 of Phosphatidylinosi	3;3;3;3	3;3;3;3	3;3;3;3	4	3	3	3
LMNB1	LMNB1	LMNB	LMNB1 Lamin-B1;>IPI:IPI00790831.1|TREMBL:Q6I	24;20	24;20	22;18	2	24	24	22
ARPC5L	ARPC5L	ARPC	ARPC5L Actin-related protein 2/3 complex subunit	2	2	2	1	2	2	2
HVCN1	HVCN1	HVCN	HVCN1 Isoform 1 of Voltage-gated hydrogen chann	3;3;2;2;2	3;3;2;2;2	3;3;2;2;2	5	3	3	3
CD79B	CD79B	CD79E	CD79B CD79B antigen isoform 3 precursor;>IPI:IPI	4;4;4;1	4;4;4;1	4;4;4;1	4	4	4	4
VIM	######	VIM Vi	VIM Vimentin	30;8;3;2;2;1;1;1;	30;8;3;2;2;1;1;1;	27;8;1;1;1;0;0;0;	13	30	30	27
SYK	SYK	SYK Is	SYK Isoform Long of Tyrosine-protein kinase SYK;	12;12;6;1;1;1;1	12;12;6;1;1;1;1	12;12;6;1;1;1;1	7	12	12	12

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ed in pink decreased upon stimulation (log2H/L≤-0.5). Proteins highlighted in green increased upon stimulation (log2H/L≥0.5).

Sequence c	Unique + razc	Unique seq	Mol. weight [kD	Sequenc	Sequence lengtl	PEP	Ratio H/L	Ratio H/L norma	Log2	Ratio H/L variab	Ratio H/L cc
0.3	0.3	0.3	426.69	3685	3685;3681;3677	0.0047325	0.024376	0.031237	fs	71.748	4
30.1	30.1	30.1	26.712	256	256	1.34E-29	0.026775	0.033238	-4.911022615	139.95	3
8.1	8.1	8.1	16.537	148	148	3.86E-22	0.050684	0.064243	-3.960316925	143.57	2
12.5	12.5	12.5	19.25	176	176;162	4.36E-06	0.05439	0.069999	-3.836521878	17.163	2
8.7	8.7	8.7	34.258	298	298;227;204;20	8.18E-05	0.06478	0.073908	-3.758125656	73.828	2
4.7	4.7	4.7	100.23	895	895;799	3.08E-06	0.80213	0.08923	-3.48632735	141.21	3
36.3	36.3	36.3	16.572	146	146	5.00E-22	0.079516	0.10072	-3.311577907	189.9	2
19.2	19.2	19.2	22.739	208	208	1.34E-15	0.10369	0.12916	-2.952768749	23.784	2
23.5	23.5	23.5	10.932	102	102;101;47	1.60E-05	1.1439	0.13134	-2.928621735	0.039896	2
19.6	19.6	19.6	57.767	511	511;511;511;51	1.51E-16	0.27273	0.34514	-1.53474641	90.521	5
12.1	12.1	12.1	44.552	412	412;379;299;27	2.52E-18	0.44198	0.55478	-0.850012316	11.855	4
8.7	8.7	8.7	27.993	264	264;236;236;23	2.43E-07	0.44853	0.56031	-0.835702854	178.03	2
7.7	7.7	7.7	42.037	390	390;344;340;15	0.0016583	0.47679	0.56117	-0.83349021	52.169	2
6.6	6.6	6.6	48.101	438	438;421;392;28	2.54E-07	0.47231	0.6026	-0.730727422	1.8233	2
1.8	1.8	1.8	267.29	2363	2363	3.20E-07	0.46869	0.6089	-0.715722782	11.299	4
6	6	4.1	71.313	637	637;636;633;53	9.67E-13	0.50779	0.6264	-0.674843882	82.819	3
17.9	17.9	17.9	82.704	732	732;131;112;19	1.10E-36	0.52234	0.65224	-0.616525175	8.5434	11
23.9	23.9	23.9	22.58	226	226;59	1.97E-37	0.55057	0.66298	-0.592962745	1.6822	7
19.9	19.9	19.9	45.46	396	396;361;321;18	1.97E-67	0.60655	0.66772	-0.582684841	14.805	7
7.1	7.1	7.1	45.357	422	422;392;400	1.13E-10	0.60623	0.67976	-0.556902625	3.3569	3
17.6	17.6	17.6	27.366	238	238;235;165;13	1.31E-11	0.5594	0.6834	-0.549197847	6.6238	6

5.2	5.2	5.2	32.749	306	306;296	6.50E-10	0.58428	0.69001	-0.535310825	18.698	2
29.6	29.6	29.6	69.842	609	609;557;559;56	1.36E-84	0.56807	0.69005	-0.535227194	7.8422	17
3.5	3.5	3.5	81.074	709	709	8.04E-14	0.55607	0.69187	-0.531427109	4.5361	2
29	29	29	27.744	248	248;292;201;14	4.12E-28	0.59943	0.70383	-0.506701086	33.342	9
35.6	35.6	35.6	21.007	188	188;94;127;166;	1.94E-29	0.57463	0.70813	-0.497913857	18.612	5
10.5	10.5	10.5	26.215	237	237	1.97E-06	0.60786	0.71182	-0.490415626	15.236	3
23.5	23.5	23.5	21.364	213	213;221;219;22	2.10E-26	0.57173	0.72153	-0.470868714	20.496	18
4.5	4.5	4.5	56.338	513	513	1.31E-07	0.57409	0.72417	-0.465599683	11.927	2
10.1	10.1	10.1	24.22	218	218;192;179;16	1.34E-07	0.58946	0.72486	-0.464225716	7.2076	2
30.6	30.6	30.6	76.613	710	710;603;482;29	1.56E-299	0.58754	0.72607	-0.461819451	12.099	44
8	8	8	35.716	313	313;279;186	2.77E-08	0.62543	0.73238	-0.449335701	3.2879	2
52.2	52.2	52.2	64.615	592	592;591;231;20	2.12E-194	0.61335	0.73377	-0.446600173	9.2719	26
41.2	41.2	41.2	26.183	228	228;223;185;14	1.64E-44	0.58023	0.73793	-0.438444126	4.2541	13
40.5	40.5	40.5	27.557	264	264	9.64E-111	0.58814	0.74322	-0.42813877	16.983	12
7.1	7.1	7.1	66.129	589	589	1.84E-10	0.621	0.74678	-0.421244805	4.8061	4
5.2	5.2	5.2	40.545	362	362;345	0.00011498	0.66375	0.75652	-0.402549872	16.265	2
5.1	5.1	5.1	24.279	217	217;196	9.97E-10	0.61137	0.76317	-0.389923634	5.6432	2
36.8	36.8	36.8	30.375	277	277;222;173;27	1.41E-75	0.60873	0.76367	-0.388978745	6.7184	6
4.7	4.7	4.7	74.746	709	709;700;699	5.17E-09	0.61872	0.76372	-0.38888429	13.704	4
14.3	14.3	14.3	88.549	835	835;753	2.28E-48	0.63265	0.78386	-0.351332088	25.87	8
39.4	39.4	39.4	37.429	353	353;317;341	5.33E-66	0.63696	0.78663	-0.346242887	48.535	16
30.5	30.5	30.5	15.936	154	154;135	4.86E-27	0.62247	0.78828	-0.343219924	5.3658	5
18.4	16.2	16.2	46.659	414	414;173;157;23	2.41E-32	0.61964	0.792	-0.336427665	29.321	6
1.2	1.2	1.2	242.04	2285	2285;2068;1902	1.39E-07	0.61984	0.7931	-0.334425312	6.5697	2
2.2	2.2	2.2	95.436	881	881;867;860;84	0.0016787	0.64607	0.79414	-0.33253473	1.5727	2
8.8	8.8	8.8	41.757	373	373;358;329;29	1.93E-12	0.63037	0.79434	-0.332171441	12.598	2
21.5	21.5	21.5	15.164	135	135;135;101	1.35E-09	0.60411	0.7946	-0.331699301	9.6839	4
7.3	7.3	7.3	30.518	260	260	0.00012954	0.63649	0.79476	-0.331408831	43.786	2

3.5	3.5	3.5	57.563	508	508;477	6.40E-07	0.63131	0.79541	-0.330229395	5.5015	2
13.5	13.5	2.5	50.679	443	443;428;425;32	6.17E-35	0.60957	0.79628	-0.328652273	7.7581	8
4.9	4.9	4.9	36.926	346	346;331;297;23	5.91E-10	0.62672	0.79659	-0.328090726	5.2415	2
8.3	8.3	8.3	27.872	240	240;240;243;24	6.63E-07	0.67646	0.79719	-0.327004482	16.302	2
2.5	2.5	2.5	132.88	1214	1214;1130;1105	2.47E-18	0.63246	0.79811	-0.325340494	13.532	3
8.4	8.4	8.4	34.534	320	320;309	3.85E-06	0.6346	0.79959	-0.322667666	5.6373	2
13.6	13.6	13.6	23.787	220	220;215;213;12	6.20E-08	0.63782	0.80202	-0.318289881	45.456	2
14.6	14.6	14.6	36.214	322	322;314;292;29	2.04E-23	0.69037	0.803	-0.316528107	3.1512	3
5.7	5.7	5.7	79.578	756	756	8.67E-05	0.64488	0.80469	-0.313494991	7.218	2
40.3	40.3	40.3	43.062	390	390;115;150	1.90E-101	0.71929	0.80954	-0.304825728	8.2724	15
9	9	9	32.854	288	288;267;145;63	8.41E-09	0.69005	0.81261	-0.299364976	4.6101	3
3.6	3.6	3.6	99.966	895	895;847;283	0.00025669	0.65023	0.81481	-0.295464409	16.154	2
3.7	3.7	3.7	27.296	243	243;203	0.015501	0.68056	0.81674	-0.292051209	12.674	2
9	9	9	35.107	312	312;297;136	5.32E-08	0.74211	0.81872	-0.288557956	9.3321	3
8.5	8.5	8.5	51.782	460	460;210;162;18	7.04E-11	0.65646	0.81958	-0.287043316	9.0249	4
13.7	13.7	13.7	65.401	586	586;579;568;56	3.38E-25	0.72776	0.82125	-0.284106629	10.235	10
14.5	14.5	14.5	25.072	228	228;190	2.42E-05	0.6621	0.82201	-0.28277215	9.7938	3
15.8	15.8	15.8	51.026	461	461;355;193	3.96E-28	0.63924	0.82325	-0.280597488	4.9633	9
11.9	11.9	11.9	24.579	218	218;218	4.58E-10	0.669	0.82442	-0.278548591	2.0309	2
8.5	8.5	8.5	90.583	825	825;806;784;72	1.35E-28	0.66755	0.82574	-0.276240502	15.204	15
3.7	3.7	3.7	72.687	668	668;520	6.39E-13	0.67769	0.82578	-0.276170617	38.926	2
19.4	19.4	19.4	38.845	372	372;320;267;32	1.07E-22	0.61422	0.82629	-0.275279887	33.382	9
48.2	5.4	5.4	49.924	448	448;433;266;19	1.74E-240	0.64528	0.82903	-0.270503786	5.34	5
24	24	24	36.726	325	325;289;69	9.75E-25	0.66941	0.82943	-0.269807865	19.037	5
18.3	18.3	18.3	19.329	164	164;124	9.00E-12	0.65182	0.83076	lk	2.3239	2
5	5	5	33.172	301	301	0.0027683	0.68565	0.83394	-0.261984506	0.39471	2
42.8	42.8	0	25.834	236	236;235;152	8.37E-163	0.67381	0.83763	-0.255614981	8.9447	19
39.1	39.1	39.1	29.032	248	248;248;232;24	3.05E-63	0.66321	0.83813	-0.254754061	5.8071	18

6	6	6	40.589	351	351;343;398;36(	4.72E-13	0.70113	0.83842	-0.254254963	0.30784	2
15	15	15	36.824	341	341;328;395	2.35E-60	0.67403	0.83899	-0.25327448	1.6654	4
10.3	10.3	10.3	59.929	532	532;494;459	1.11E-19	0.66737	0.84002	-0.251504418	4.556	5
5.5	5.5	5.5	67.699	604	604;593;590;55	5.71E-05	0.70966	0.84098	-0.249856604	0.78016	2
13.9	13.9	13.9	45.796	403	403;389;389;18(	2.83E-66	0.76697	0.84141	-0.249119131	11.069	5
54.8	54.8	48.1	45.26	418	418;364	3.52E-205	0.74635	0.84239	-0.247439785	11.623	42
7	7	7	42.467	385	385;356;282;23(	1.79E-13	0.71772	0.84334	-0.245813711	4.8745	2
9.5	9.5	9.5	59.004	524	524;510;504;37	2.03E-34	0.68715	0.84336	-0.245779498	7.2478	6
10.6	3.5	3.5	71.048	604	604;583	1.85E-17	0.68125	0.84658	-0.240281689	35.96	2
21.7	21.7	21.7	25.476	221	221;209;201;19	8.76E-37	0.70524	0.84666	-0.240145364	8.0749	7
7.9	7.9	7.9	44.468	378	378	1.93E-26	0.66997	0.8476	-0.238544507	3.4252	3
5	5	5	34.092	301	301;276;233	7.48E-10	0.70177	0.84776	-0.238272198	0.69644	2
8.9	8.9	8.9	44.503	416	416;386;197	2.87E-57	0.70935	0.84907	-0.236044596	17.282	4
5.2	5.2	5.2	82.285	734	734;733;691;41	1.36E-08	0.67767	0.84909	-0.236010613	8.0665	3
12.5	12.5	12.5	31.359	280	280;277;224;22	5.32E-11	0.68021	0.84947	-0.235365097	9.2478	3
9.3	9.3	9.3	28.17	268	268;257;237;22	3.68E-25	0.68501	0.85001	-0.234448281	8.5932	2
20.4	20.4	20.4	29.909	260	260;252	3.72E-34	0.71887	0.85063	-0.233396358	5.7514	4
14.9	14.9	14.9	41.694	368	368;355;329;32	4.12E-12	0.6759	0.85172	-0.231548867	7.5804	4
9.1	9.1	9.1	35.249	317	317;314;298;29	1.64E-16	0.72433	0.85209	-0.230922275	8.7611	2
2.6	2.6	2.6	124	1114	1114;1104;1058	4.49E-08	0.67513	0.85438	-0.227050219	6.1508	3
11.8	11.8	11.8	30.84	305	305	8.34E-26	0.72628	0.8552	-0.225666242	7.3302	2
17.7	17.7	17.7	47.046	434	434;433;422	1.60E-63	0.67341	0.85675	-0.223053808	7.4466	5
11.7	5.8	5.8	46.871	411	411;97;96;91;77	5.18E-29	0.66736	0.85727	-0.222178437	6.9691	2
3.8	3.8	3.8	107.77	1010	1010;433;101	5.44E-14	0.68943	0.85729	-0.22214478	3.4649	7
13	13	13	25.357	239	239;190;114	9.14E-11	0.69716	0.85916	-0.219001268	6.093	3
17	11.5	11.5	22.541	200	200	1.73E-16	0.68534	0.86018	-0.217289507	3.8106	3
5.5	5.5	5.5	38.792	348	348;320	8.27E-06	0.77099	0.8635	-0.211731917	13.85	3
5	5	5	106.9	954	954;904	5.23E-25	0.70337	0.86599	-0.207577729	5.8578	5

42.2	42.2	42.2	62.639	543	543;590;519	4.56E-126	0.7243	0.86704	-0.205829543	13.548	30
9.8	9.8	9.8	19.108	174	174;148	0.00025513	0.68978	0.86733	-0.205347083	5.2128	2
12.1	12.1	12.1	35.845	315	315;195;186;16(	1.43E-14	0.69678	0.86753	-0.205014447	13.165	5
35.9	35.9	35.9	40.411	357	357;339;219;19-	1.42E-106	0.68287	0.86781	-0.204548884	42.811	16
13.1	13.1	10.3	31.279	282	282	7.10E-08	0.71096	0.86984	-0.201178042	9.444	5
19.5	19.5	19.5	56.65	533	533;499	2.58E-60	0.69514	0.87193	-0.197715777	3.4325	10
24.2	24.2	24.2	33.824	302	302	4.88E-27	0.71974	0.87205	-0.197517239	10.616	8
5.6	5.6	5.6	43.448	392	392;386;385;37!	2.60E-08	0.7813	0.873	-0.195946441	9.3178	2
58.8	58.8	58.8	18.012	165	165;129;105;12:	3.53E-129	0.68235	0.87492	-0.192776988	8.0234	51
12.7	12.7	12.7	22.519	197	197;179;171;15(	7.09E-07	0.69007	0.87608	-0.190865478	0.40973	2
29.3	29.3	29.3	38.242	331	331;282;211;20!	6.54E-34	0.75421	0.87707	-0.189236104	5.8178	12
31.8	31.8	31.8	38.655	352	352;210;169;22:	3.71E-120	0.72362	0.87819	-0.187394988	8.8622	14
5.4	5.4	5.4	59.717	542	542;537;533;48:	1.87E-25	0.71057	0.87821	-0.187362133	4.572	4
33.1	33.1	33.1	18.648	172	172;297;263;16!	1.95E-60	0.71364	0.87943	-0.185359347	93.496	3
2.6	2.6	2.6	115.58	1097	1097;1082;1081	2.22E-05	0.69581	0.88055	-0.183523168	28.74	3
7.3	7.3	7.3	63.826	561	561;545;515;50!	1.01E-06	0.70937	0.88138	-0.182163935	12.584	3
18	11.8	11.8	48.408	451	451;336;287;14!	9.62E-128	0.76862	0.8817	-0.181640235	11.823	5
54.5	49	49	21.892	198	198;183;136;14:	6.02E-102	0.70273	0.88205	-0.181067656	8.0335	21
42	35.1	35.1	27.764	245	245;149	1.74E-147	0.67954	0.88269	-0.180021241	5.8357	8
3.9	3.9	3.9	280.74	2647	2647;2639;2607	2.50E-22	0.68136	0.88335	-0.178942921	5.4496	7
13	13	13	29.841	253	253	1.71E-06	0.74669	0.8837	-0.178371411	5.5886	3
12.2	12.2	12.2	95.907	853	853;808;330	1.44E-33	0.71672	0.88392	-0.178012292	9.6749	8
8.5	8.5	8.5	35.943	330	330;309;270	2.63E-19	0.74223	0.88411	-0.177702216	8.0089	4
2.4	2.4	2.4	52.562	455	455;368	0.0028981	0.69532	0.88434	-0.177326949	21.351	2
13.7	13.7	13.7	82.588	737	737	8.80E-58	0.68044	0.88446	-0.177131197	8.8894	6
21.6	21.6	21.6	95.785	858	858;835	1.90E-92	0.71603	0.88508	-0.176120232	7.5249	15
47.2	47.2	2.5	47.958	432	432	6.67E-211	0.70727	0.88546	-0.175500959	10.27	37
9.6	9.6	9.6	38.388	333	333;327	2.88E-31	0.69567	0.88549	-0.17545208	63.724	3

15.1	15.1	15.1	44.991	416	416;295;298;26(	3.01E-23	0.69301	0.88567	-0.175158843	3.6158	4
51.6	7.4	7.4	49.585	444	444;362;236	1.53E-252	0.68956	0.88597	-0.174670247	4.6225	3
7.8	7.8	7.8	25.734	231	231	7.97E-08	0.70156	0.8861	-0.174458573	8.5137	2
10.4	10.4	10.4	92.888	821	821;83	1.78E-30	0.71813	0.88625	-0.174214373	9.7498	9
14.6	3	3	75.491	694	694	2.69E-56	0.7124	0.8866	-0.173644732	1.2942	2
31.4	31.4	29.1	73.114	711	711;710;364	8.79E-88	0.71193	0.88701	-0.172977726	5.2101	23
12.7	7	7	51.229	472	472;449;449;40	1.30E-83	0.701	0.88719	-0.172684991	13.459	3
56.4	56.4	45	17.302	149	149;174;86;116;	6.55E-54	0.68275	0.88742	-0.172311027	14.122	14
23.2	23.2	23.2	59.632	557	557;550;531;32	1.84E-77	0.71832	0.88867	-0.170280309	3.8469	11
17.5	17.5	17.5	23.934	212	212;154;122	3.65E-10	0.7019	0.88887	-0.169955659	3.4603	3
29.7	29.7	29.7	28.264	256	256;240;233;26	3.31E-45	0.68851	0.88941	-0.169079469	8.9912	9
10.7	10.7	10.7	26.056	233	233	9.98E-08	0.7599	0.88986	-0.168349717	20.064	2
13.7	13.7	13.7	33.186	300	300;283;154;14	7.32E-15	0.70942	0.88991	-0.168268657	7.9809	2
12.1	12.1	12.1	24.95	224	224	1.53E-05	0.76025	0.89026	-0.167701359	8.7096	2
6.8	6.8	6.8	96.557	863	863;823	7.77E-17	0.72215	0.89123	-0.166130298	5.7136	4
16	16	16	33.67	306	306;293;288;25(	8.46E-37	0.71415	0.89131	-0.166000803	4.7143	5
36	36	36	12.203	111	111;110;109;10	2.08E-51	0.66609	0.89237	-0.164286082	7.7121	6
11.7	11.7	9.8	43.171	409	409;403;80	3.25E-29	0.71085	0.89258	-0.163946614	4.6284	5
37.6	37.6	37.6	24.488	218	218;261;216;19	5.49E-32	0.71952	0.89392	-0.161782369	5.8692	8
39.8	3.8	0	25.773	236	236	1.47E-156	0.70858	0.89499	-0.160056532	0.59755	2
15.5	15.5	15.5	50.808	438	438;436;436;38	6.84E-68	0.68572	0.89615	-0.15818786	8.3058	6
46.1	3.3	3.3	49.679	451	451	8.37E-222	0.70471	0.89653	-0.157576235	0.8314	2
6.8	6.8	6.8	38.996	353	353;326	1.07E-10	0.7123	0.89749	-0.156032231	2.9471	2
9	9	9	38.449	346	346;299;299	1.41E-12	0.78642	0.89807	-0.155100195	13.485	2
0.8	0.8	0.8	213.47	2080	2080;2035;1966	0.00013293	0.70076	0.89852	-0.154377478	14.35	2
31.6	31.6	31.6	18.042	158	158;112;80;158;	1.61E-25	0.69846	0.8989	-0.153767466	7.6142	4
12.3	12.3	12.3	30.692	268	268;220;165;14	6.99E-08	0.77468	0.89893	-0.153719318	3.2814	4
27.2	27.2	27.2	14.57	136	136;86;135;135;	2.16E-25	0.71087	0.90023	-0.151634452	13.513	4

3.9	3.9	3.9	42.153	407	407;386	6.59E-10	0.75388	0.90026	-0.151586375	19.412	2
18.4	18.4	18.4	16.859	147	147	1.35E-12	0.6876	0.90068	-0.150913469	0.24094	2
73.8	73.8	73.8	21.057	187	187;196;155;65;	2.65E-174	0.70286	0.90072	-0.150849399	4.5287	17
24.2	24.2	24.2	26.706	252	252;252;229;16	9.82E-20	0.7227	0.90169	-0.149296573	11.55	9
6.9	6.9	6.9	69.284	611	611;537;508;29	5.30E-22	0.77415	0.90283	-0.147473736	10.736	3
18.6	18.6	18.6	28.772	253	253;233	1.61E-05	0.67998	0.90284	-0.147457757	6.1598	2
8.1	8.1	8.1	53.376	528	528;525;524;52	3.11E-31	0.78962	0.90534	-0.143468398	10.474	7
18.8	18.8	18.8	40.763	368	368;337	8.42E-21	0.71431	0.90551	-0.143197521	6.7077	7
1.8	1.8	1.8	117.97	1052	1052;389;340	0.00017441	0.71593	0.90601	-0.142401121	1.4711	2
11.4	11.4	11.4	51.294	474	474;351;176;15	3.60E-10	0.70536	0.90622	-0.142066764	5.4999	5
31	31	28.7	38.434	355	355;306;336;28	2.92E-60	0.76893	0.90686	-0.141048249	19.551	17
4.6	4.6	4.6	33.879	307	307	0.001696	0.74637	0.90756	-0.13993507	12.107	2
42	42	42	19.398	169	169;168;129;81;	5.81E-47	0.7215	0.90785	-0.139474148	9.9001	16
23.4	23.4	23.4	35.18	308	308;271;315	1.48E-71	0.77088	0.90872	-0.138092263	2.3729	10
16.2	16.2	16.2	51.156	463	463;255	9.44E-39	0.71681	0.90898	-0.137679543	9.0149	10
9.5	9.5	9.5	32.613	294	294;249;125;30	6.63E-16	0.71109	0.90977	-0.136426233	8.0937	4
26.4	26.4	17.7	37.497	356	356	2.60E-90	0.79483	0.90994	-0.136156675	5.8675	15
6.8	6.8	6.8	40.542	367	367;235	7.86E-16	0.78693	0.91012	-0.135871317	11.917	2
41	41	41	22.406	200	200;157;139;14	8.95E-64	0.72888	0.91019	-0.135760359	8.731	6
9.9	9.9	9.9	18.762	162	162;140;172;17	0.0016735	0.69768	0.91024	-0.135681109	20.308	2
22.5	22.5	21.4	76.149	707	707;669	5.81E-103	0.72557	0.91026	-0.13564941	11.017	28
11.8	11.8	11.8	29.816	271	271;263;183;20	0.00010715	0.72793	0.91075	-0.134873005	2.3441	2
5.6	5.6	5.6	47.46	429	429;387;119;72;	1.94E-10	0.70906	0.911	-0.134477041	0.57268	2
16.2	16.2	16.2	45.199	427	427;162	3.19E-26	0.81512	0.91131	-0.133986196	10.254	7
32.5	32.5	32.5	29.999	268	268;238	6.33E-36	0.70549	0.91404	-0.129670793	10.037	9
16.7	7.3	7.3	21.429	192	192;185;148;16	3.18E-17	0.72097	0.91419	-0.129434057	7.7694	2
12.3	12.3	12.3	123.8	1134	1134;1066;491;	5.58E-60	0.72048	0.9158	-0.12689553	13.473	10
6.4	6.4	6.4	57.398	517	517;217	2.49E-15	0.72665	0.91581	-0.126879777	1.6765	3

4.1	4.1	4.1	115.96	1041	1041	5.69E-08	0.72377	0.91593	-0.12669075	4.2216	3
3.8	3.8	3.8	31.75	291	291;257;236;148	9.31E-07	0.75437	0.91607	-0.126470251	6.2852	2
24.9	24.9	19.7	28.585	249	249;247;209;245	1.43E-18	0.72877	0.91628	-0.126139565	7.6447	9
23.6	23.6	23.6	29.597	263	263;263;263;267	6.26E-13	0.73386	0.91652	-0.125761732	27.429	8
37.9	37.9	37.9	20.455	182	182	3.42E-24	0.73893	0.91709	-0.124864773	2.3701	6
9.2	9.2	9.2	35.117	315	315;296;265;204	4.36E-26	0.72827	0.91727	-0.124581639	9.1448	2
27.3	16.8	16.8	25.145	238	238;238;129;125	1.48E-111	0.72815	0.91815	-0.123198226	6.8058	7
17.3	17.3	17.3	42.613	376	376;335;376;147	2.92E-60	0.80245	0.91879	-0.12219294	12.276	7
11.2	11.2	11.2	35.611	320	320;144	2.33E-30	0.79683	0.91904	-0.121800441	8.5375	3
43.8	43.8	43.8	51.028	464	464;463;440;439	4.23E-179	0.74951	0.91907	-0.121753348	22.969	24
46.6	46.6	46.6	13.527	118	118;117;108;117	4.13E-53	0.72575	0.92022	-0.119949283	10.678	6
13.6	13.6	13.6	34.559	309	309;182	2.42E-31	0.72518	0.92173	-0.117583887	16.942	4
1.8	1.8	1.8	134.5	1233	1233;1220;1205	7.01E-10	0.72849	0.92191	-0.117302178	27.784	2
21.1	18.5	18.5	33.729	303	303;152;111	4.12E-14	0.78778	0.92201	-0.117145697	9.0652	4
36.8	36.8	36.8	22.876	204	204;107	2.19E-115	0.74849	0.92244	-0.116473021	7.5409	8
53.3	53.3	53.3	18.898	165	165;174;172;176	2.77E-40	0.72007	0.92312	-0.115409893	8.8335	14
11.1	11.1	11.1	32.872	289	289;288;288;70	3.67E-12	0.80041	0.92338	-0.11500361	7.9636	6
10.9	10.9	10.9	60.626	534	534;431;306;162	4.28E-06	0.76116	0.92348	-0.114847378	6.2412	3
17.2	17.2	17.2	38.274	338	338	2.97E-26	0.83752	0.92657	-0.110028123	33.292	5
7.4	7.4	7.4	34.746	312	312;230	1.47E-05	0.74166	0.92692	-0.109483266	13.613	2
9.3	9.3	9.3	65.596	605	605;412;162	1.03E-23	0.74646	0.92705	-0.109280943	3.4965	5
39	39	39	33.313	300	300;295;264;295	4.49E-173	0.76067	0.92728	-0.108923056	7.5044	19
24.2	24.2	24.2	65.688	599	599;490;490;488	1.14E-73	0.74133	0.92729	-0.108907498	15.836	43
22.3	22.3	22.3	49.203	439	439	1.17E-60	0.72537	0.92789	-0.107974309	14.479	9
32.4	32.4	32.4	17.276	148	148;146;102;91;	3.30E-10	0.72115	0.92811	-0.107632291	13.396	4
71.3	71.3	71.3	28.85	254	254;254;253;254	9.04E-152	0.73603	0.92885	-0.10648246	13.158	30
3.2	3.2	3.2	122.34	1162	1162;1162;1132	1.96E-17	0.73427	0.92922	-0.105907889	5.0463	4
8	8	8	68.965	661	661;656;655;618	2.60E-21	0.74511	0.9293	-0.105783687	4.5061	4

27.8	27.8	27.8	110.5	1020	1020;935	3.53E-159	0.75524	0.92939	-0.105643973	19.996	39
26	26	8.4	50.67	454	454;414;378;34	7.55E-68	0.77286	0.92939	-0.105643973	13.245	15
1.8	1.8	1.8	189.56	1678	1678;1632;1280	2.00E-06	0.75315	0.92991	-0.104837001	7.0628	4
7.6	7.6	7.6	42.981	381	381	1.02E-23	0.71673	0.92998	-0.104728405	10.074	2
13.7	13.7	13.7	41.581	366	366;352;106;56;	8.23E-09	0.80316	0.93015	-0.104464705	9.6098	3
11	11	11	42.502	374	374;123	1.18E-29	0.81369	0.93022	-0.104356136	12.769	4
7.1	7.1	7.1	76.715	693	693;594	1.91E-12	0.74724	0.93084	-0.103394887	1.1425	2
5.9	5.9	5.9	223.69	2017	2017;129	4.59E-35	0.73891	0.93244	-0.1009172	6.0729	10
3.3	3.3	3.3	80.62	764	764;639;638;62	8.97E-10	0.7418	0.93249	-0.100839841	15.374	3
16.5	16.5	16.5	25.177	224	224	1.01E-11	0.74698	0.93262	-0.100638726	7.516	3
25.4	25.4	25.4	82.999	763	763;260	5.33E-89	0.74917	0.93276	-0.100422173	8.9597	15
10.3	10.3	10.3	123.38	1071	1071;1070;179;	6.02E-30	0.75797	0.93296	-0.100112867	10.283	8
6	6	6	51.355	452	452	2.36E-08	0.79995	0.93296	-0.100112867	8.8384	2
23.2	14.8	14.8	38.651	366	366;365;362;36	2.82E-83	0.78989	0.93312	-0.09986547	10.284	8
22.7	22.7	22.7	269.76	2541	2541;2542;261	2.64E-245	0.73939	0.93349	-0.099293527	10.391	35
11.3	11.3	11.3	45.908	397	397;391;391;38	4.68E-18	0.80882	0.93387	-0.098706362	9.2936	4
4.9	4.9	4.9	115.75	1051	1051;1030;1009	1.29E-08	0.75281	0.93445	-0.097810624	12.757	3
40.1	40.1	40.1	32.66	289	289;178;240	2.63E-79	0.77683	0.93476	-0.097332095	7.4624	15
28.9	28.9	28.9	25.895	232	232;219;189;18	3.95E-55	0.74862	0.93487	-0.097162332	7.132	7
17.7	17.7	17.7	33.58	305	305;119;212	6.63E-15	0.78769	0.93514	-0.096745728	3.5767	3
31.8	31.8	31.8	27.547	258	258;200	2.34E-50	0.7404	0.93527	-0.096545183	1.9966	4
6.5	6.5	6.5	99.028	873	873;814;302;15	4.72E-24	0.73982	0.9355	-0.096190441	4.9629	4
55.2	55.2	55.2	16.06	145	145	1.21E-54	0.72035	0.9356	-0.096036233	13.559	14
7	7	7	35.576	314	314;172;122	4.45E-08	0.79674	0.93576	-0.095789534	13.795	2
16.7	9.3	9.3	28.218	246	246;72;39	1.70E-39	0.73792	0.93617	-0.095157561	1.1723	2
3.6	3.6	3.6	55.18	504	504	2.01E-05	0.74905	0.9363	-0.094957237	26.62	2
4.6	4.6	4.6	55.011	504	504;313;298;28	5.01E-15	0.78819	0.93641	-0.094787754	3.4601	2
35.6	35.6	35.6	46.247	413	413;366	7.37E-62	0.82592	0.93729	-0.093432604	5.4497	12

14.1	14.1	14.1	21.397	184	184;184;282;18	6.66E-06	0.76119	0.93805	-0.092263271	3.2935	2
1.2	1.2	1.2	101.3	890	890;874;874;69	0.0058755	0.75086	0.93863	-0.091371523	1.1072	2
1.8	1.8	1.8	109.93	963	963	0.00058788	0.74257	0.93972	-0.089697141	0.33421	2
17.2	17.2	17.2	36.573	325	325;147	3.42E-22	0.73942	0.93983	-0.089528275	18.984	5
37.7	37.7	37.7	36.071	329	329	5.38E-55	0.75918	0.94005	-0.089190601	6.4693	14
70.4	70.4	70.4	26.688	243	243;186;133;11	2.12E-77	0.75346	0.94093	-0.087840696	10.189	27
7	6.4	6.4	180.61	1575	1575;1071;1071	3.18E-48	0.75284	0.94102	-0.087702709	7.0968	8
6.1	6.1	6.1	35.206	329	329;295;243;20	6.48E-06	0.75285	0.94106	-0.087641386	1.2984	2
9.1	9.1	9.1	28.279	263	263;230;214;19	2.07E-07	0.76142	0.94119	-0.087442103	1.3996	2
19.5	19.5	16.1	65.308	589	589;534;555;50	3.51E-37	0.79184	0.94143	-0.087074268	34.947	18
12.3	12.3	12.3	28.315	268	268	6.69E-08	0.75325	0.94183	-0.086461418	0.18731	3
6.8	6.8	6.8	91.838	790	790;141	6.85E-17	0.75107	0.94198	-0.086231666	3.8746	4
27.7	27.7	27.7	13.281	119	119;119	3.81E-34	0.74268	0.94328	-0.084242016	7.3401	6
11.1	11.1	11.1	21.676	198	198;183;155;69	1.83E-06	0.76597	0.94394	-0.083232935	20.28	2
21.2	21.2	21.2	31.324	293	293;293;290;18	5.97E-30	0.79032	0.94439	-0.08254533	10.869	11
1.8	1.8	1.8	76.28	659	659;483	1.10E-09	0.79257	0.94467	-0.082117652	4.5371	2
57	57	57	25.831	235	235;204;249;19	3.60E-51	0.72139	0.94657	-0.079218896	20.227	10
6.5	6.5	6.5	49.973	461	461	1.25E-56	0.73695	0.94682	-0.078837914	2.3663	2
23.4	23.4	17.5	18.11	154	154;153	1.49E-14	0.74583	0.94686	-0.078776966	9.3817	3
27.7	27.7	27.7	70.901	607	607;564;531;46	3.19E-101	0.7876	0.94688	-0.078746493	10.015	13
12.1	4.7	4.7	67.819	577	577;576;141;20	3.78E-20	0.78188	0.94691	-0.078700785	16.753	2
17.6	17.6	15.1	45.374	391	391;383;368;32	2.72E-46	0.76163	0.9474	-0.077954423	7.4527	16
23.2	23.2	23.2	10.839	95	95;95;91;71;147	1.18E-19	0.72618	0.94742	-0.077923967	3.0605	2
22.2	22.2	22.2	22.591	194	194;113;194;15	5.08E-14	0.76413	0.94787	-0.077238887	5.6207	6
13.9	13.9	13.9	26.599	245	245;226;108	2.19E-19	0.75244	0.94812	-0.076858428	13.579	4
9.2	9.2	9.2	31.7	273	273;271;271;16	1.47E-06	0.8049	0.94822	-0.076706272	12.399	2
23.5	23.5	23.5	59.755	527	527	2.87E-40	0.7487	0.94833	-0.076538919	11.536	8
31.6	31.6	31.6	31.462	282	282;253;230	6.34E-32	0.80577	0.94843	-0.076386797	4.642	8

3.4	3.4	3.4	51.556	437	437;428;166	3.09E-06	0.77083	0.94848	-0.076310742	0.15673	2
20.3	20.3	20.3	81.307	719	719;543;389;18	2.52E-83	0.74792	0.94855	-0.076204272	5.7718	12
39.9	39.9	39.9	18.431	158	158;161	5.26E-16	0.74319	0.94907	-0.075413596	25.096	7
8.5	8.5	8.5	113.08	1014	1014;250	1.35E-36	0.752	0.9491	-0.075367993	6.0456	9
3.7	3.7	3.7	77.515	730	730;691	3.01E-08	0.76713	0.95081	-0.072771018	2.7577	2
11.1	11.1	11.1	88.885	793	793;728;259;23	2.08E-51	0.77746	0.95108	-0.072361397	11.859	6
2.8	2.8	2.8	82.387	762	762;686	0.00221	0.75469	0.9511	-0.072331059	1.9729	2
3.5	3.5	3.5	98.398	889	889;434	1.29E-10	0.77202	0.95124	-0.072118713	14.731	2
20.8	20.8	20.8	29.945	264	264;264;263;14	1.73E-30	0.77113	0.95154	-0.07166379	6.192	9
25	25	11.4	26.528	236	236;233;191;13	2.50E-22	0.7725	0.95203	-0.070921059	5.5324	7
21.8	15.4	15.4	33.929	298	298;264;238;25	1.56E-16	0.81335	0.95244	-0.070299884	8.4224	3
39.6	39.6	39.6	47.716	432	432;404	5.29E-60	0.75088	0.95329	-0.069012932	11.767	31
12.1	12.1	12.1	59.143	528	528	3.58E-21	0.77668	0.95336	-0.068906999	6.4183	6
5.3	5.3	5.3	90.577	830	830;780;400	2.39E-08	0.76663	0.95343	-0.068801074	16.32	4
21.7	20	20	54.231	471	471;382;235;20	7.58E-26	0.7566	0.95353	-0.068649766	8.4239	9
11.8	11.8	11.8	82.593	744	744;739;563;40	1.13E-23	0.77599	0.95377	-0.06828669	39.865	7
6.1	6.1	6.1	27.349	246	246;232;209;15	1.48E-15	0.76879	0.95382	-0.068211061	4.4613	2
8.2	8.2	8.2	39.594	352	352;351;307	3.20E-05	0.81202	0.95384	-0.06818081	6.5142	2
20	16.5	8	70.051	641	641;641;586;41	3.84E-93	0.79871	0.95454	-0.06712244	3.2074	9
62.2	62.2	62.2	47.168	434	434;341;434;43	0	0.75501	0.95498	-0.066457576	10.54	102
36.5	36.5	36.5	35.554	318	318;150	5.62E-66	0.74114	0.95503	-0.066382042	6.3072	15
10.8	10.8	10.8	112.92	995	995;966;847;31	9.88E-27	0.77412	0.95532	-0.065944027	12.264	9
49.2	42.3	38.6	28.082	246	246;244;100;74	1.13E-151	0.76475	0.95561	-0.065506144	17.253	10
5.9	5.9	5.9	74.797	666	666;599;552;19	2.75E-20	0.79475	0.95588	-0.065098579	19.112	4
44.9	44.9	44.9	22.026	214	214;162;170;12	4.75E-52	0.7447	0.95722	-0.063077554	4.6604	10
27.1	27.1	27.1	35.076	317	317;221;153;16	1.12E-93	0.80177	0.95723	-0.063062483	26.283	16
14.9	14.9	14.9	23.593	208	208;208;208;25	1.26E-12	0.7657	0.95728	-0.062987127	8.7115	3
64.3	64.3	52.8	22.11	199	199;171;97	1.25E-86	0.75572	0.95777	-0.062248848	14.19	32

19.7	19.7	19.7	20.9	183	183	4.96E-11	0.7721	0.95781	-0.062188597	14.28	3
20.1	20.1	20.1	33.395	299	299	2.58E-35	0.80665	0.95788	-0.062083164	3.07	5
53.3	53.3	53.3	28.768	261	261	1.45E-121	0.76609	0.95803	-0.061857261	10.785	19
9.1	9.1	9.1	136.31	1204	1204;1204;645;(	5.22E-80	0.75048	0.95815	-0.061676565	8.4772	13
19.4	19.4	10.9	23.467	211	211;192;148;19:	4.90E-14	0.77452	0.95835	-0.061375455	2.8548	4
7.6	7.6	7.6	94.68	925	925;215;219;16	1.44E-114	0.79557	0.95911	-0.060231808	5.224	9
17.5	17.5	17.5	71.407	647	647;646;281;25	2.40E-155	0.81411	0.95913	-0.060201724	8.3083	16
77.7	77.7	77.7	18.502	166	166;112;166	5.24E-219	0.75977	0.96048	-0.058172522	6.8574	24
13.9	13.9	13.9	18.795	173	173	2.73E-07	0.7476	0.96094	-0.057481741	7.4194	2
10.9	10.9	10.9	52.739	488	488;466;434	5.76E-28	0.75257	0.96108	-0.057271569	25.591	6
64.6	20.4	16.9	47.766	426	426;464;372;31	0	0.77022	0.96235	-0.055366407	26.026	31
15.1	5.6	5.6	20.828	179	179;168	4.46E-17	0.75915	0.96258	-0.055021647	6.1763	2
41.7	41.7	41.7	14.515	132	132;133	1.76E-85	0.73888	0.96399	-0.052909914	3.5695	8
19.3	19.3	19.3	33.488	290	290;277;268;26	4.46E-46	0.78956	0.96431	-0.052431086	6.8628	8
40	40	40	117.85	1058	1058;603;506;2	0	0.76727	0.9649	-0.051548662	49.44	73
6.8	6.8	6.8	68.997	585	585;527	1.01E-09	0.80679	0.96491	-0.051533711	8.5481	4
7.5	7.5	7.5	80.109	704	704;495	9.97E-32	0.78323	0.96492	-0.051518759	15.656	6
18.1	18.1	18.1	20.838	193	193;186	1.93E-34	0.76011	0.96499	-0.051414103	11.751	5
83.6	83.6	83.6	19.891	189	189	1.08E-102	0.77029	0.96535	-0.05087599	10.337	21
46.1	46.1	46.1	17.138	152	152;144;153;94;	7.82E-31	0.73814	0.96553	-0.050607009	5.131	7
11.3	11.3	11.3	21.916	194	194;158;158;15(	1.97E-14	0.78363	0.96575	-0.050278322	1.4175	3
1.5	1.5	1.5	273.6	2335	2335	5.58E-08	0.75508	0.96614	-0.049695835	2.0955	2
42.8	42.8	42.8	22.988	201	201;185;182;11	8.23E-49	0.74793	0.96725	-0.048039271	10.287	8
20.3	20.3	20.3	42.592	380	380	7.12E-81	0.75324	0.96759	-0.047532236	8.3829	8
2	2	2	150.83	1337	1337;1297;600	2.07E-16	0.7646	0.96761	-0.047502416	3.3094	2
6.5	6.5	6.5	39.149	369	369;322	5.44E-06	0.81143	0.96761	-0.047502416	3.4943	2
4.8	4.8	4.8	39.157	354	354;320	7.44E-10	0.80085	0.96838	-0.046354811	6.8778	2
27.6	27.6	27.6	42.671	377	377;378	2.78E-54	0.85768	0.96854	-0.046116463	22.244	10

12	12	12	20.457	184	184;158	7.71E-05	0.74257	0.9688	-0.04572923	2.2414	3
20.3	20.3	20.3	33.232	295	295	4.14E-23	0.81825	0.96892	-0.045550542	18.644	5
63	63	63	24.65	227	227;286;285;19	1.49E-139	0.75456	0.96929	-0.044999728	7.5177	38
14.3	14.3	14.3	44.819	406	406;314;236;11	6.94E-86	0.762	0.96965	-0.044464002	15.958	4
5.1	5.1	5.1	83.353	739	739	1.34E-09	0.78369	0.97005	-0.043868984	3.872	3
14.4	14.4	14.4	100.2	908	908;778;749;59	2.66E-44	0.78565	0.97041	-0.043333677	5.3243	11
75	75	75	15.054	140	140;140	1.47E-100	0.74428	0.97103	-0.042412226	18.242	18
13.2	13.2	13.2	67.314	599	599	1.01E-47	0.84692	0.97104	-0.042397369	14.905	7
26.6	26.6	26.6	43.786	394	394;372;406;18	3.77E-35	0.76761	0.97115	-0.042233949	4.114	9
15.2	15.2	15.2	44.965	408	408;402;393;38	6.34E-81	0.77236	0.97138	-0.041892312	3.8744	8
65	65	65	57.936	531	531;605;531;51	0	0.77733	0.97148	-0.0417438	46.579	133
26.2	26.2	26.2	31.362	282	282;178;145	6.51E-89	0.75275	0.97265	-0.040007338	12.288	6
17.2	17.2	17.2	14.21	122	122	1.20E-05	0.7673	0.97291	-0.039621742	19.963	2
2.1	2.1	2.1	144.72	1338	1338;1338	0.001937	0.76594	0.97359	-0.038613745	6.3733	2
26	26	26	56.166	519	519;488;358	2.66E-65	0.78288	0.9737	-0.038450753	9.7615	13
17.4	17.4	17.4	29.062	258	258;204	9.92E-18	0.75086	0.97373	-0.038406304	9.1422	4
12.1	12.1	12.1	24.49	206	206;162	0.00013417	0.79119	0.97385	-0.038228521	2.9548	2
46.2	46.2	46.2	20.17	184	184;154;154;15	2.52E-40	0.74817	0.97422	-0.037680494	6.9898	11
17.9	12.7	12.7	28.787	251	251;195;156	3.25E-15	0.76932	0.97438	-0.037443574	24.648	7
30.9	30.9	30.9	50.227	456	456;386;267;19	6.83E-65	0.7687	0.97473	-0.036925447	7.7864	17
39.2	39.2	39.2	14.463	125	125;130;128;12	1.33E-14	0.76819	0.97525	-0.036156002	2.7368	3
46.2	46.2	46.2	89.321	806	806;160;115	3.06E-220	0.78206	0.97542	-0.035904541	18.228	50
21.2	21.2	21.2	37.432	335	335	4.58E-26	0.7917	0.97628	-0.034633119	8.5425	10
12.4	12.4	9.1	40.816	372	372;370;339;25	2.86E-30	0.76526	0.97694	-0.033658135	10.596	5
79.7	79.7	79.7	30.791	286	286;249;210;24	1.39E-198	0.76987	0.97713	-0.03337758	8.7207	32
19.5	19.5	19.5	49.184	440	440;294;244;41	1.36E-36	0.78087	0.97767	-0.032580511	5.6567	6
17.6	17.6	11.1	45.671	415	415;159;355	2.44E-77	0.77103	0.97797	-0.032137885	10.499	8
13.2	13.2	13.2	32.418	273	273;272;259;24	1.36E-22	0.78388	0.97854	-0.031297269	7.3423	5

7.4	7.4	7.4	145.83	1304	1304	8.79E-25	0.7755	0.97862	-0.031179328	91.783	7
23.9	23.9	23.9	16.005	142	142;119;61;59;4	7.03E-18	0.76035	0.97902	-0.030589763	1.3872	6
1.9	1.9	1.9	157.18	1401	1401;939;394;1	1.41E-09	0.77626	0.97957	-0.029779504	11.069	2
45.9	45.9	45.9	16.445	146	146;146;152	1.73E-23	0.75438	0.98001	-0.029131624	7.4966	14
10.7	10.7	9.1	48.162	419	419;408;393;27	8.19E-60	0.7731	0.98018	-0.028881385	14.251	4
13.8	13.8	13.8	38.534	356	356;311;181	1.87E-45	0.86236	0.98051	-0.028395751	8.3492	4
23.3	23.3	23.3	292.74	2671	2671;140	3.41E-274	0.76224	0.98098	-0.027704371	12.566	59
39.4	39.4	39.4	34.273	317	317;278;255;31	7.37E-101	0.81771	0.98118	-0.027410268	5.1135	17
7.3	7.3	7.3	37.359	331	331	0.00029642	0.77557	0.98159	-0.026807543	3.4554	2
26.5	26.5	26.5	64.324	569	569;558;532;55	1.02E-115	0.78561	0.98171	-0.026631184	9.3514	20
15.5	15.5	15.5	20.762	187	187;152;149;14	1.23E-10	0.73639	0.9819	-0.026351992	4.7042	2
2.2	2.2	2.2	57.46	500	500;474;294;20	0.017986	0.81251	0.98216	-0.025970027	6.0503	4
54	54	54	36.053	335	335;335;293;36	1.16E-173	0.79054	0.98261	-0.025309173	8.866	132
2.1	2.1	2.1	152.78	1360	1360;1068	1.16E-08	0.77874	0.98271	-0.025162358	0.090212	2
9	9	9	29.995	266	266;266;191;15	9.88E-10	0.83128	0.9829	-0.02488345	0.70809	2
21.6	21.6	21.6	18.254	153	153;145;110;14	8.10E-09	0.79106	0.98325	-0.024369814	3.9252	4
18.9	18.9	18.9	166.57	1382	1382	2.09E-111	0.78447	0.98331	-0.02428178	9.1802	26
23.7	23.7	23.7	23.897	215	215;181	2.97E-39	0.79792	0.98332	-0.024267108	8.8725	5
13.8	13.8	13.8	47.697	427	427;414;250;23	5.68E-13	0.74767	0.9841	-0.023123171	5.0465	5
51	51	51	17.222	151	151	2.19E-28	0.77529	0.98426	-0.02288863	7.1919	9
9.5	9.5	9.5	58.075	525	525;580;565;55	1.35E-07	0.79329	0.98428	-0.022859315	6.8733	5
29.9	29.9	29.9	17.84	164	164;163;134	2.99E-15	0.79874	0.98434	-0.022771373	4.0088	3
22.2	22.2	22.2	20.762	176	176;154;176;14	3.13E-17	0.79622	0.98456	-0.022448967	5.2452	4
1.9	1.9	1.9	166.17	1487	1487;1478;1460	0.00034748	0.78774	0.98463	-0.022346398	2.2939	2
59.6	59.6	2.7	49.83	445	445;397;447;44	6.62E-301	0.77564	0.98508	-0.021687202	33.949	103
51.1	51.1	51.1	20.777	184	184	1.70E-47	0.78969	0.9851	-0.021657911	6.3842	14
10.9	10.9	10.9	18.829	175	175;126;120	4.92E-09	0.75573	0.98597	-0.020384344	3.4525	3
19.5	19.5	19.5	19.148	169	169;163;137;87;	1.46E-11	0.78314	0.98626	-0.019960072	9.809	6

19.8	19.8	19.8	41.331	369	369;359;146;24(	1.61E-50	0.78405	0.98663	-0.01941894	8.6589	10
19.3	19.3	11.9	69.412	586	586;586	6.13E-36	0.78975	0.98734	-0.018381119	8.9102	17
54.1	54.1	54.1	22.782	205	205;171;186	2.52E-79	0.79035	0.98787	-0.017606894	28.983	12
24.3	24.3	24.3	28.415	255	255;175;154;14	6.02E-22	0.78605	0.98848	-0.016716319	7.9076	4
43.6	43.6	43.6	14.865	140	140;140;122;11	1.08E-58	0.75882	0.99001	-0.014484997	3.242	7
19.1	19.1	19.1	35.594	309	309;309;309	1.11E-12	0.82571	0.99013	-0.014310137	16.677	5
7.3	7.3	7.3	37.154	328	328;326;278	1.71E-11	0.82243	0.99028	-0.014091592	8.7084	2
9.5	9.5	9.5	140.47	1264	1264;1264;366;2	4.45E-35	0.78266	0.99046	-0.013829382	15.02	12
8	8	8	78.839	689	689;258	9.16E-13	0.78347	0.99123	-0.012708243	12.248	5
36.1	11.9	11.9	37.186	327	327;138;125	6.33E-83	0.76796	0.99133	-0.012562704	9.7821	3
8.9	8.9	8.9	35.853	316	316;263;102;46	3.58E-07	0.79383	0.99135	-0.012533598	19.352	3
65.2	65.2	65.2	25.035	224	224;101	1.72E-93	0.79117	0.99162	-0.012140725	10.289	22
50.3	50.3	28.5	83.263	724	724;597;168;50	0	0.78818	0.99168	-0.012053435	21.843	172
24	24	24	13.742	125	125;124;63	1.38E-14	0.76014	0.99172	-0.011995244	4.5202	5
31.6	31.6	31.6	30.239	269	269;263;263;16	1.65E-25	0.78126	0.99176	-0.011937056	2.1452	7
18.4	18.4	18.4	22.04	207	207;155;165	6.93E-08	0.7774	0.99217	-0.011340759	0.86484	2
19	19	19	33.269	311	311	4.68E-20	0.79016	0.99221	-0.011282597	5.4434	4
18.8	18.8	18.8	24.205	208	208;188	4.76E-37	0.7874	0.99325	-0.009771207	3.0178	3
5.7	5.7	3.3	104.61	949	949;942;942;93	5.39E-25	0.80561	0.99344	-0.009495258	10.223	5
6.9	6.9	6.9	109.96	962	962;98	4.86E-33	0.80818	0.9937	-0.00911773	2.9522	5
37.1	37.1	37.1	16.273	151	151;350	7.86E-25	0.75981	0.99374	-0.009059657	6.4572	7
47.5	47.5	47.5	28.068	244	244;244	1.38E-61	0.79248	0.99375	-0.00904514	8.8702	10
13.3	13.3	13.3	23.466	196	196;196	2.49E-09	0.78985	0.99376	-0.009030622	3.5521	2
15.5	13	13	44.078	386	386;375;196;17	1.84E-26	0.79982	0.99384	-0.008914486	12.196	4
5.6	5.6	5.6	226.53	1960	1960;1382;2036	6.17E-56	0.76506	0.99392	-0.00879836	6.13	8
17.8	17.8	17.8	14.997	129	129;125;40	1.77E-12	0.76944	0.99423	-0.008348459	7.0955	2
28.9	28.9	28.9	24.261	211	211;211;101	6.23E-37	0.78744	0.99432	-0.008217869	7.5106	6
15.5	15.5	15.5	17.911	161	161;118;113	7.95E-08	0.76995	0.99489	-0.007391072	4.1946	2

18.1	18.1	18.1	20.457	177	177;172;171;15	4.89E-14	0.79939	0.99498	-0.007260568	3.1299	3
17.4	17.4	17.4	22.151	195	195;177;162;11	6.68E-14	0.80455	0.9951	-0.007086582	6.6083	2
7.5	7.5	7.5	105.84	953	953;922;192	2.57E-35	0.78961	0.99526	-0.006854633	5.7872	7
61.9	61.9	61.9	44.614	417	417;327;281;41	5.72E-246	0.77555	0.99533	-0.006753167	9.417	46
6.5	6.5	6.5	61.312	536	536;514	1.90E-07	0.79003	0.99584	-0.006014129	1.7998	3
65.5	65.5	62.4	29.174	255	255;193;139;26	1.18E-187	0.77594	0.99678	-0.004652973	8.1173	31
6.3	5.1	5.1	69.993	666	666;655;654;64	9.67E-11	0.7919	0.99687	-0.004522717	4.5201	3
20.7	20.7	17.9	36.748	324	324;286;220	1.29E-37	0.85137	0.99697	-0.004378002	6.0378	5
29.7	19.6	19.6	24.033	209	209	1.28E-26	0.76313	0.99705	-0.00426224	19.813	7
20.9	20.9	20.9	12.985	115	115;115;115;28	1.47E-20	0.77506	0.99749	-0.003625717	5.0057	2
21.6	21.6	21.1	189.25	1657	1657;1631	3.48E-221	0.79063	0.9977	-0.00332202	18.044	41
34.5	34.5	28.6	46.153	406	406;408;407;36	2.86E-73	0.77443	0.99844	-0.002252362	9.2566	20
34.2	34.2	34.2	24.763	225	225;123;68;224;	1.23E-60	0.79494	0.99863	-0.001977847	6.6445	6
0.9	0.9	0.9	242.98	2225	2225;2162;280	1.18E-06	0.76924	0.99937	-0.000909184	12.015	2
64.8	64.8	64.8	17.818	165	165;132;117	9.72E-90	0.79317	0.99955	-0.000649359	5.6241	16
16.8	16.8	16.8	39.681	363	363;336;303;19	4.56E-47	0.78801	0.99976	-0.000346288	9.7168	5
43.7	43.7	43.7	50.118	437	437;487;437;20	4.02E-107	0.78392	1.0003	0.000432744	6.9517	27
8.1	8.1	8.1	17.745	161	161	5.87E-08	0.76677	1.0004	0.000576963	1.6366	2
3.3	3.3	3.3	135.65	1197	1197;1099	1.85E-08	0.78395	1.0009	0.001297842	18.131	3
15.7	15.7	15.7	36.501	325	325;125	3.82E-18	0.80177	1.0012	0.001730196	3.0751	6
20	20	20	33.112	290	290;188;186;93	1.91E-13	0.84572	1.0012	0.001730196	5.4438	3
21.8	21.8	21.8	28.836	248	248;201;201;20	1.92E-17	0.80121	1.0013	0.001874286	8.4405	4
28.9	28.9	28.9	57.116	508	508;452;279;22	4.53E-45	0.80551	1.0013	0.001874286	6.89	13
5.5	5.5	5.5	469.08	4128	4128;4097;4096	1.02E-126	0.7887	1.0016	0.002306467	7.682	19
17.5	4	4	49.122	422	422	2.28E-80	0.79889	1.0016	0.002306467	3.1292	8
53.1	45.7	42	27.745	245	245;170;98;92	4.11E-233	0.79956	1.0016	0.002306467	7.9875	14
22.3	22.3	22.3	52.878	475	475;391;248;17	7.80E-38	0.80441	1.0019	0.00273852	7.8582	17
29.4	29.4	8.5	22.171	201	201;201;201	3.11E-17	0.80573	1.002	0.002882509	13.256	7

38.2	38.2	38.2	284.54	2472	2472;2452;2477	0	0.78588	1.0023	0.003314389	11.718	89
32.2	32.2	32.2	51.804	459	459	2.99E-91	0.79334	1.0024	0.00345832	10.971	11
11.5	11.5	11.5	51.922	442	442;389;351;35(	1.25E-10	0.85946	1.0027	0.003890027	4.1353	5
14.1	14.1	14.1	34.063	313	313;291	1.07E-13	0.79254	1.0031	0.004465437	68.242	5
53.8	53.8	53.8	59.62	548	548;547;323;10	1.57E-149	0.80426	1.0033	0.004753055	8.7354	36
48.3	48.3	24.7	50.14	462	462;462;441;39	4.32E-139	0.79587	1.0034	0.004896843	39.465	94
19.7	19.7	19.7	20.252	178	178;177;174;13	6.23E-36	0.7866	1.004	0.005759269	11.805	4
54.4	54.4	54.4	26.21	228	228;201;200;13	2.83E-88	0.76795	1.0042	0.00604663	4.0806	12
25	25	25	21.634	188	188;137	1.08E-37	0.80647	1.0045	0.006477564	3.4944	5
7.7	7.7	5.7	69.147	614	614;544	5.60E-15	0.83317	1.005	0.007195501	6.9174	5
12.1	12.1	12.1	33.712	305	305;222;190;99	1.17E-13	0.86014	1.005	0.007195501	1.8242	3
5.5	5.5	5.5	52.904	456	456;436	2.50E-21	0.78984	1.0056	0.008056555	1.3992	2
14	14	14	89.656	793	793;775;764;72	2.59E-45	0.81164	1.006	0.008630305	9.3295	10
17.2	17.2	17.2	57.136	501	501;182;176;18	8.41E-38	0.76134	1.0061	0.008773707	10.863	7
3.2	3.2	2.1	111.02	1037	1037;1023;395;3	3.16E-10	0.84502	1.0061	0.008773707	15.379	4
11.6	11.6	11.6	45.566	398	398;364	2.04E-25	0.90142	1.007	0.010063683	4.0468	3
26.8	26.8	26.8	29.815	261	261;239;216;86	1.17E-44	0.85706	1.0072	0.010350188	13.7	6
1.4	1.4	1.4	211.33	1843	1843;571;1729	7.64E-10	0.80211	1.0074	0.010636636	12.45	2
8.1	8.1	8.1	48.633	433	433;130	5.12E-10	0.78507	1.008	0.011495639	8.6888	3
14	14	14	37.039	336	336;312;269	1.76E-12	0.78964	1.0081	0.011638756	12.651	4
22.2	22.2	22.2	29.483	261	261;235;237;23(	4.09E-18	0.80212	1.0083	0.011924948	10.442	7
17.6	17.6	17.6	68.996	647	647;542;225	6.75E-21	0.85056	1.0084	0.012068023	23.807	8
40.1	36.5	36.5	36.638	334	334;232;137	2.97E-95	0.83884	1.0085	0.012211084	8.717	43
40.6	40.6	40.6	25.206	217	217;176;163;15(	2.29E-28	0.80795	1.0086	0.01235413	10.109	11
23.6	23.6	23.6	16.368	148	148;141;139	2.73E-22	0.79474	1.009	0.012926174	7.8528	3
62	62	55.8	34.778	303	303;297;240;25	1.98E-97	0.85302	1.0092	0.013212111	20.236	17
5.2	5.2	5.2	35.776	309	309	1.33E-05	0.79414	1.0094	0.013497992	13.731	2
14.1	14.1	14.1	47.655	425	425;410;469;42	8.77E-35	0.78891	1.0095	0.013640911	9.4203	9

24.7	24.7	24.7	18.237	166	166	9.23E-05	0.79536	1.0097	0.013926706	27.964	3
47.7	47.7	42.9	70.897	646	646;494;493;21(	0	0.82562	1.0101	0.014498127	47.66	113
21.8	21.8	21.8	83.139	739	739;685;77	2.72E-93	0.80572	1.0104	0.014926544	13.157	15
45.2	45.2	45.2	51.153	449	449;445;400;26:	1.44E-121	0.79529	1.0112	0.016068369	30.4	25
28.7	5.2	5.2	50.47	463	463;444;340	1.70E-83	0.76118	1.0119	0.017066724	0.1309	2
52.1	52.1	42.3	24.893	215	215;216;158;16:	4.57E-79	0.78872	1.0119	0.017066724	7.6428	30
58.1	58.1	58.1	17.259	148	148;159;135;12:	1.27E-75	0.77574	1.0121	0.017351842	5.8041	11
12	12	12	21.868	191	191;191;189	2.74E-14	0.81789	1.0122	0.017494379	2.5857	2
34	34	34	59.67	541	541;486;283	1.62E-90	0.83529	1.0129	0.018491749	14.242	23
46.8	46.8	46.8	55.992	504	504;483;494;44:	3.33E-215	0.79713	1.0134	0.019203734	10.846	49
34.5	34.5	34.5	22.127	194	194;187;194;17(	6.11E-62	0.80818	1.0134	0.019203734	6.3631	11
13.8	13.8	13.8	62.293	572	572;686;619;57:	5.07E-15	0.86174	1.0139	0.019915368	9.6011	5
8.8	8.8	8.8	28.68	249	249;218;79	0.00072785	0.81929	1.0149	0.021337583	4.15	2
21.1	21.1	21.1	13.459	114	114	1.45E-21	0.79989	1.0155	0.02219024	0.42783	2
9.7	9.7	9.7	24.831	217	217;217;133	8.39E-14	0.79004	1.0161	0.023042393	9.0175	2
5.6	5.6	5.6	57.791	517	517;508;508;49:	3.16E-06	0.81991	1.0166	0.023752136	13.008	2
10.3	10.3	10.3	112.42	998	998;978;977;97(	3.92E-50	0.79983	1.0167	0.023894043	8.2064	8
17.9	17.9	17.9	23.545	212	212;216;213;18:	9.14E-22	0.82505	1.0167	0.023894043	133.08	3
53.3	53.3	53.3	17.718	152	152;152;143;34	2.38E-46	0.78401	1.0168	0.024035935	4.6864	13
68.6	68.6	68.6	24.454	220	220;199;187;13-	1.58E-158	0.82127	1.0174	0.024886999	5.6152	24
51	51	51	26.922	241	241;162	6.96E-105	0.81472	1.0181	0.025879273	6.0216	10
9.3	9.3	9.3	32.43	289	289;137;133;13:	5.46E-08	0.80223	1.0185	0.02644598	9.1931	5
8.2	8.2	2.7	51.855	475	475;474;477;45:	7.01E-45	0.81907	1.0186	0.026587622	13.764	3
4.8	4.8	4.8	16.323	147	147;126	0.013265	0.84278	1.0186	0.026587622	13.457	3
7.9	7.9	7.9	56.084	522	522	1.72E-10	0.80922	1.0188	0.026870865	8.2914	4
9.2	9.2	9.2	50.8	456	456;419	1.42E-13	0.91489	1.0189	0.027012465	2.5623	4
33.9	33.9	33.9	14.395	127	127;73;127	7.68E-38	0.76912	1.0191	0.027295624	3.5571	6
19.4	19.4	19.4	32.575	294	294;265;259;18(	2.26E-92	0.82648	1.0191	0.027295624	12.826	25

2.7	2.7	2.7	88.568	789	789	0.001538	0.82917	1.0191	0.027295624	0.49467	2
20.6	20.6	20.6	25.059	218	218	6.50E-43	0.82899	1.0201	0.028710586	9.8901	4
6.6	6.6	6.6	86.267	790	790;788;449;42	1.01E-30	0.83862	1.0203	0.028993412	8.2528	7
14.2	14.2	14.2	28.993	261	261;53;53	6.41E-15	0.81681	1.0205	0.029276182	9.8312	3
2.6	2.6	2.6	126.34	1133	1133;1107;1011	5.01E-07	0.79944	1.0207	0.029558897	3.9839	3
28.6	28.6	28.6	28.433	255	255;248	6.13E-41	0.80779	1.0211	0.030124161	12.794	7
22.8	22.8	22.8	60.533	545	545;544;507;27	1.63E-54	0.841	1.0219	0.031254025	13.059	19
18.8	18.8	18.8	14.787	128	128;95;80	1.72E-15	0.79501	1.0232	0.033088169	0.34608	2
9.6	9.6	9.6	72.932	645	645;166	7.67E-21	0.81573	1.0233	0.033229161	5.986	5
2.6	2.6	2.6	138.6	1248	1248;1192;990;	1.52E-06	0.80523	1.0235	0.033511102	22.656	2
19.6	19.6	19.6	28.825	271	271	1.72E-22	0.81483	1.0239	0.03407482	10.412	3
10.2	10.2	10.2	21.119	186	186;176;172;15	3.86E-08	0.82837	1.0249	0.035483152	6.5616	2
5.2	2.2	2.2	73.584	667	667;603;601;60	7.69E-13	0.86529	1.0255	0.036327492	0.8352	2
29.1	29.1	29.1	19.448	165	165;163;160;13	4.92E-36	0.80901	1.0258	0.036749476	15.722	8
5.5	5.5	5.5	106.49	959	959;923;763	2.63E-16	0.83384	1.0265	0.037733627	20.882	6
2.8	2.8	2.8	29.946	283	283	0.0052599	0.80692	1.0269	0.038295698	3.7243	2
4.2	4.2	4.2	61.626	552	552;511;423;18	4.17E-06	0.82387	1.0271	0.038576651	15.795	2
23.5	23.5	23.5	61.397	558	558;558;299	3.39E-38	0.81352	1.0274	0.038997979	8.3767	8
54.8	54.8	54.8	15.55	135	135;136;135;98;	3.32E-86	0.78773	1.0277	0.039419183	6.2129	9
10.3	10.3	10.3	176.23	1606	1606;1600;1600	7.90E-57	0.81824	1.0278	0.039559557	13.157	12
32	32	32	157.9	1394	1394;531;504;3	1.30E-276	0.8064	1.028	0.039840265	34.209	56
38.9	38.9	38.9	22.367	198	198;198;121;11	1.42E-44	0.82736	1.0287	0.04082231	4.3407	7
11	11	11	25.855	228	228;181;179;16	0.00021755	0.83365	1.0288	0.040962548	24.996	2
8.9	8.9	8.9	49.149	428	428;414;195	7.81E-16	0.86158	1.029	0.041242982	4.7972	3
19.1	19.1	19.1	37.482	335	335;272;277;26	4.94E-35	0.87184	1.0291	0.041383179	7.0146	10
45.8	45.8	45.8	57.488	535	535;130	1.02E-220	0.83256	1.0292	0.041523362	10.405	34
15.3	15.3	15.3	91.706	796	796;363	3.11E-68	0.81877	1.0293	0.041663532	4.4547	11
26.2	26.2	26.2	59.366	543	543;499;501;45	6.31E-128	0.83955	1.0293	0.041663532	6.0539	21

29.4	29.4	29.4	52.22	445	445;172	9.87E-51	0.80161	1.0294	0.041803688	7.0276	14
22	22	22	14.551	123	123;96;99	8.43E-24	0.75552	1.0296	0.042083959	4.0122	3
59.6	59.6	58.4	95.337	858	858;566;151	0	0.82443	1.0299	0.042504263	9.6051	126
14.6	14.6	14.6	33.969	301	301;301;287;28(	7.39E-10	0.82459	1.0303	0.043064479	5.831	4
16.9	16.9	16.9	16.648	154	154	5.43E-22	0.80112	1.031	0.044044333	5.7672	2
40.9	40.9	38.9	50.909	452	452;419	2.17E-130	0.8021	1.032	0.045442971	11.471	21
41.4	41.4	41.4	26.227	227	227;105	2.86E-33	0.80971	1.0322	0.045722536	5.1295	10
16.9	16.9	16.9	48.275	419	419;353;348;10(	2.85E-23	0.82197	1.0322	0.045722536	5.5699	8
12.5	12.5	12.5	15.798	136	136;80;40	8.28E-07	0.80226	1.0325	0.046141782	0.58025	2
43.8	43.8	43.8	14.839	130	130;388;129	4.05E-14	0.80395	1.0327	0.046421211	11.15	7
28.4	28.4	28.4	24.74	215	215	1.07E-44	0.8255	1.0327	0.046421211	10.55	6
37.1	37.1	34.5	96.864	858	858;814;860;81	3.52E-202	0.84626	1.0361	0.051163253	8.276	37
20.2	20.2	20.2	101.11	900	900;635;254;90;	4.20E-73	0.83993	1.0363	0.051441711	8.4277	15
6	6	6	177.19	1555	1555;1531;131	1.13E-28	0.82216	1.0366	0.051859299	8.5323	6
42.7	42.7	42.7	25.898	234	234;164;48;36	1.42E-41	0.84148	1.0368	0.052137623	5.3358	12
19.5	19.5	19.5	170.6	1512	1512;988	8.63E-79	0.82685	1.037	0.052415894	69.576	26
16	16	16	34.324	312	312;98	1.31E-13	0.85135	1.0374	0.052972275	8.1388	4
15.2	15.2	15.2	39.548	349	349;1186;1129;:	7.45E-27	0.9301	1.0382	0.054084393	3.1906	3
20.9	20.9	20.9	39.611	350	350;257;217	3.14E-38	0.87413	1.0383	0.054223347	11.31	8
5	5	5	82.431	740	740	0.00076473	0.83309	1.0386	0.054640131	6.4861	2
4.7	4.7	4.7	71.368	634	634;586;578;50	5.63E-06	0.87332	1.0392	0.055473336	2.464	3
17.6	17.6	17.6	51.712	466	466;431;421;27:	3.30E-21	0.80906	1.0393	0.055612157	13.835	9
11.1	11.1	11.1	36.112	315	315	6.13E-33	0.82498	1.0398	0.05630606	6.3394	4
18.8	18.8	9.7	37.377	340	340;147;108;13-	9.52E-24	0.82779	1.0403	0.05699963	13.983	8
37.4	37.4	37.4	22.168	206	206;162;107	1.22E-19	0.84106	1.0406	0.057415612	6.0781	6
4.1	4.1	4.1	98.063	870	870;870;866;86(	2.85E-07	0.84912	1.0409	0.057831475	18.994	3
36.6	36.6	36.6	20.811	183	183;101;62	4.91E-29	0.84493	1.0412	0.058247217	7.3812	3
27.6	27.6	27.6	57.924	539	539;514;493	1.13E-77	0.83641	1.0415	0.058662839	5.9342	23

7.1	7.1	7.1	37.025	324	324	3.13E-16	0.90069	1.0416	0.058801354	1.1536	2
17.2	17.2	17.2	21.863	192	192;168;165;14	4.87E-57	0.83399	1.0417	0.058939855	7.0876	3
9.4	9.4	9.4	102.35	898	898;890;848;88	5.18E-32	0.84927	1.042	0.059355278	13	7
4.9	4.9	4.9	105.47	914	914;913;792;76	2.46E-25	0.83164	1.0421	0.059493725	6.0452	6
13.3	13.3	13.3	45.626	406	406;398;345;89	2.75E-28	0.80544	1.0427	0.060324133	2.6325	4
51.2	51.2	47.9	39.837	361	361;332;332;33	4.08E-189	0.86095	1.0429	0.06060083	12.476	81
5.6	5.6	5.6	41.738	373	373;341;245;19	3.51E-07	0.91255	1.0443	0.06253622	13.267	2
14.1	14.1	14.1	21.994	199	199;193;193;18	5.64E-24	0.83938	1.0447	0.063088712	12.978	3
70	70	70	23.356	210	210;174;52	0	0.83197	1.0459	0.06474492	4.2514	28
28.8	28.8	28.8	22.949	205	205;112;107	2.71E-61	0.83893	1.048	0.067638717	2.793	5
8.1	8.1	8.1	81.673	737	737;732;518;30	1.86E-15	0.83453	1.0481	0.067776372	10.362	5
10.2	10.2	10.2	25.646	226	226;186;182;91	5.20E-06	0.84748	1.0481	0.067776372	5.0177	3
35.3	35.3	35.3	26.411	241	241	1.11E-51	0.83591	1.0488	0.068739591	14.858	8
12.2	12.2	12.2	21.229	189	189;189;188;18	4.72E-05	0.85165	1.0494	0.069564695	3.5562	2
18.2	18.2	5.9	35.924	324	324;322;374;36	3.06E-68	0.82922	1.0497	0.06997707	6.0197	5
9.2	9.2	9.2	41.079	380	380;377;203;86	2.17E-05	0.81768	1.0499	0.070251922	14.461	2
43.3	43.3	43.3	22.836	201	201;249	5.54E-38	0.83826	1.0507	0.071350804	10.183	8
37.5	37.5	37.5	29.204	264	264	1.44E-29	0.85281	1.051	0.071762669	11.188	5
13.7	13.7	13.7	70.67	636	636;636;547;60	2.94E-47	0.84888	1.0514	0.07231164	31.857	9
27.1	27.1	26.7	274.61	2364	2364;2168;2155	0	0.81811	1.0518	0.072860402	10.699	66
2	2	2	142.08	1283	1283;1278;1278	3.68E-06	0.83668	1.0523	0.073546061	7.2204	2
54.5	6	3.1	50.135	451	451;450;415;38	0	0.82609	1.0524	0.073683154	4.4505	2
50	50	50	27.887	248	248;178;191;25	3.10E-121	0.82844	1.0535	0.075190314	6.0929	12
14.5	14.5	14.5	41.024	365	365;333	2.63E-19	0.88474	1.0536	0.075327251	10.399	5
10.4	10.4	10.4	83.677	758	758;747;726;71	1.20E-37	0.84663	1.0537	0.075464174	7.2614	7
8.5	8.5	8.5	54.889	484	484;745;498;42	3.84E-08	0.84959	1.055	0.077242999	15.835	4
29	29	29	110.42	971	971;945;762;56	2.33E-239	0.8581	1.0553	0.077653186	9.1112	27
22.7	22.7	22.7	60.343	556	556;401	5.81E-71	0.87797	1.0566	0.079429315	56.833	14

3.9	3.9	3.9	140.96	1270	1270	2.61E-10	0.83189	1.057	0.079975377	5.7158	5
16	16	16	18.658	163	163;168;160	8.41E-21	0.85783	1.0572	0.08024833	7.383	3
1.3	1.3	1.3	226.25	2039	2039;2032;1972	2.34E-09	0.83816	1.0577	0.080930488	7.1882	3
26.6	26.6	26.6	58.024	531	531;486;530;49	7.74E-145	0.85829	1.0578	0.08106688	6.2937	15
15.3	15.3	15.3	16.442	144	144;144;144;11	3.99E-08	0.83561	1.0582	0.081612323	6.1072	3
15.5	15.5	15.5	26.707	238	238;151;151;14	1.62E-19	0.81136	1.0586	0.082157559	1.3467	3
3.6	3.6	3.6	72.777	646	646;121	2.58E-11	0.88484	1.0588	0.0824301	9.6661	2
41.1	41.1	41.1	23.489	207	207;160;150;11	9.16E-125	0.8485	1.0592	0.082975027	14.915	7
12.5	12.5	12.5	19.41	168	168;157;150;12	2.45E-16	0.8604	1.0603	0.084472517	9.5735	3
6.1	6.1	6.1	63.541	587	587;312	5.17E-09	0.88704	1.0612	0.085696581	13.718	2
44.1	44.1	44.1	26.409	236	236;233;216;23	4.71E-75	0.84871	1.0619	0.086647913	11.952	40
39	39	39	26.489	241	241;196	2.52E-43	0.85914	1.0635	0.088820033	7.4342	10
33.2	33.2	33.2	37.54	337	337	1.86E-58	0.84251	1.0638	0.089226942	22.787	23
4.9	4.9	4.9	27.978	247	247	1.13E-06	0.85368	1.0639	0.089362553	7.6647	2
32.9	32.9	32.9	53.139	483	483;429;289	1.37E-96	0.82052	1.0645	0.09017595	13.29	16
12.4	12.4	12.4	47.366	418	418;414;387	4.11E-29	0.80956	1.0652	0.091124334	6.5506	3
12	12	12	136.37	1230	1230;1062;403	8.79E-73	0.83734	1.0653	0.091259766	32.311	11
26.4	26.4	26.4	34.93	307	307	7.23E-24	0.89227	1.0653	0.091259766	11.956	11
3.4	3.4	3.4	69.725	616	616;616;587;57	0.0033399	0.85074	1.0677	0.094506339	1.9465	2
16.8	16.8	16.8	51.721	469	469;458;457;23	2.82E-34	0.85323	1.0677	0.094506339	23.712	6
13.7	13.7	13.7	24.146	204	204;174;186;17	1.21E-08	0.85238	1.0679	0.094776557	5.9862	3
22.8	22.8	22.8	55.804	514	514;470;279;24	2.39E-52	0.8463	1.0684	0.095451881	8.7416	10
69.6	69.6	69.6	11.665	115	115	1.22E-81	0.79437	1.0686	0.095721922	3.3295	6
5.8	5.8	5.8	35.744	325	325;324;308;27	1.37E-11	0.8559	1.0692	0.096531743	3.9513	2
6.1	6.1	6.1	107.14	953	953	1.69E-13	0.86677	1.07	0.097610797	5.6673	5
55.3	55.3	55.3	12.774	114	114	3.59E-32	0.82082	1.0709	0.098823768	9.271	5
47.4	47.4	47.4	32.551	293	293	7.24E-67	0.86038	1.0711	0.099093179	17.137	17
26.2	26.2	26.2	27.385	248	248;294	1.17E-21	0.84136	1.0718	0.100035721	2.5765	3

7.7	7.7	7.7	46.48	416	416;409;289	4.24E-14	0.83642	1.074	0.102993993	9.365	3
7.3	7.3	7.3	30.375	275	275;224;215;13	2.51E-05	0.8653	1.0746	0.103799743	11.313	2
9	9	9	21.612	188	188;179;167;13	1.13E-05	0.84652	1.0747	0.103933991	15.47	2
27.2	27.2	27.2	20.825	184	184;184;184;13	3.57E-48	0.8721	1.0747	0.103933991	6.2294	5
2.2	2.2	0.8	97.621	871	871;401	3.44E-07	0.87477	1.0754	0.104873377	22.648	3
2.5	2.5	2.5	126.97	1140	1140;1009;826;4	7.34E-07	0.84988	1.0755	0.105007525	7.8093	3
34.5	19.8	19.8	98.16	854	854;732;539;34	0	0.85223	1.0765	0.10634832	10.816	65
6.6	6.6	6.6	32.816	302	302;285	6.51E-13	0.8596	1.0777	0.10795563	16.124	2
29.3	29.3	29.3	27.399	246	246;227;272	6.01E-37	0.86301	1.078	0.108357178	9.1395	8
22.4	22.4	22.4	49.874	455	455	1.36E-53	0.8308	1.079	0.109694865	3.417	10
31.3	31.3	31.3	17.162	163	163	1.04E-08	0.83123	1.079	0.109694865	0.81081	3
0.8	0.8	0.8	482.14	4376	4376;4374;4365	3.84E-07	0.85777	1.0809	0.112233058	10.199	3
19.2	19.2	19.2	35.079	333	333;284;229	4.39E-36	0.89495	1.0815	0.113033665	6.0126	7
6	6	6	28.777	248	248;237;217;21	0.00089159	0.8664	1.0824	0.114233744	3.6168	2
32.3	32.3	32.3	39.146	372	372;357;348	7.46E-141	0.84263	1.0825	0.114367025	5.7282	8
43.6	43.6	26	20.697	181	181;181;173;14	1.48E-64	0.83681	1.0834	0.115565996	7.8017	15
7.9	7.9	7.9	27.735	241	241;232;227;22	8.60E-08	0.86413	1.0842	0.116630912	23.8	2
5.9	5.9	5.9	88.67	803	803;400;396;36	5.13E-10	0.86199	1.0854	0.118226814	5.9154	3
11.8	11.8	11.8	55.52	491	491;368;241;47	1.74E-26	0.87377	1.0866	0.119820952	7.6461	4
3.6	3.6	3.6	117.97	1019	1019;464	4.69E-10	0.88263	1.0869	0.120219212	21.251	4
46.5	46.5	46.5	15.945	142	142	2.00E-16	0.84974	1.087	0.12035194	1.2749	5
22.3	22.3	22.3	53.165	471	471;430;109	1.19E-69	0.86452	1.0892	0.123268887	3.2296	7
12.6	12.6	12.6	34.577	310	310	1.73E-13	0.8855	1.0898	0.124063396	3.9739	4
25.3	25.3	25.3	30.588	285	285;332;329;28	3.39E-44	0.87392	1.0912	0.125915549	19.717	8
28.1	28.1	21	56.782	505	505;461;147;72	1.79E-38	0.84195	1.0919	0.126840735	7.5728	13
64	64	18.5	32.642	292	292;267;152;13	2.45E-72	0.81537	1.0932	0.128557365	7.0325	25
33.8	33.8	14.5	16.363	145	145;103;149;10	9.98E-15	0.8379	1.0932	0.128557365	21.303	5
41.4	41.4	41.4	28.723	249	249;250	7.16E-99	0.86759	1.0934	0.128821281	9.0381	19

17.8	17.8	17.8	26.836	241	241;195;192;13	1.77E-21	0.88255	1.0941	0.129744606	18.268	2
3.6	3.6	3.6	50.388	467	467;339;277;27	4.10E-89	0.86021	1.0942	0.129876461	14.898	2
15.5	15.5	15.5	75.378	660	660;588	9.08E-30	0.90642	1.0945	0.130271955	5.7661	7
27.3	27.3	27.3	12.538	110	110;94;57;55	2.71E-08	0.80342	1.0949	0.130799111	8.7618	3
5.9	5.9	5.9	50.464	456	456;353	2.50E-22	0.86169	1.0952	0.131194352	8.4786	2
56.5	7.9	7.9	19.653	177	177;152;85	2.91E-50	0.84022	1.0962	0.13251104	1.9103	2
8.4	8.4	8.4	144.5	1262	1262;1055;229;	4.13E-52	0.87042	1.0984	0.135403531	8.3287	15
8.1	8.1	8.1	21.819	198	198;156	1.45E-15	0.89195	1.0984	0.135403531	2.2871	2
44.4	44.4	44.4	12.855	108	108;129	1.23E-28	0.83598	1.0994	0.136716384	6.2989	5
17.8	17.8	17.8	24.976	219	219;177	9.23E-10	0.89396	1.1016	0.139600465	10.511	5
44.4	44.4	44.4	26.477	239	239;232;224;20	5.33E-45	0.88237	1.102	0.140124224	7.0949	12
30.8	30.8	27.3	32.922	286	286;276	3.04E-107	0.85772	1.1022	0.140386032	14.756	10
26.1	26.1	26.1	30.241	264	264	2.94E-29	0.87555	1.1023	0.140516919	4.949	5
19.6	19.6	19.6	96.771	873	873;868;271;23	2.59E-70	0.89304	1.1024	0.140647793	7.112	12
15.3	15.3	15.3	28.048	261	261;123	2.07E-17	0.87898	1.1027	0.141040345	1.1589	2
32	30.3	30.3	92.468	803	803;553;163;45	1.08E-141	0.89527	1.1034	0.141955886	7.6236	22
13.7	13.7	13.7	103.28	919	919;478;163;26	6.55E-31	0.90056	1.1036	0.142217362	21.481	11
48.1	48.1	48.1	23.742	216	216;178	3.61E-67	0.87792	1.1039	0.142609487	14.656	19
20.8	20.8	20.8	47.534	423	423;160	3.19E-38	0.8681	1.1052	0.144307467	12.699	7
7.7	7.7	7.7	15.807	143	143	1.27E-21	0.87218	1.1055	0.144699025	3.8833	2
24.4	24.4	24.4	53.9	492	492;440	3.08E-87	0.85481	1.1062	0.145612247	74.109	13
4.1	4.1	4.1	118.32	1094	1094	6.94E-10	0.86777	1.1079	0.147827668	3.5817	3
24.6	24.6	24.6	109.29	992	992;968	2.63E-80	0.8903	1.1079	0.147827668	4.5133	23
68.9	68.9	68.9	19.608	180	180;134;30	2.51E-53	0.87685	1.108	0.147957881	9.9066	11
3.3	3.3	3.3	122.41	1104	1104;1100;1093	7.33E-20	0.87563	1.1081	0.148088083	8.2776	3
23.3	23.3	23.3	97.169	876	876;660	6.40E-147	0.89858	1.1086	0.148738913	6.4123	36
15.1	15.1	15.1	25.05	238	238;207	7.64E-53	0.89365	1.1115	0.152507948	8.6138	2
31.3	31.3	31.3	12.784	115	115;115;96;56;5	2.13E-23	0.87759	1.1141	0.155878733	3.0545	3

3.3	3.3	3.3	101.27	866	866;865;864;53(	4.11E-07	0.90874	1.116	0.158337027	4.6934	3
8.1	8.1	8.1	30.111	273	273;227;227;22	2.23E-05	0.87914	1.1161	0.158466295	1.947	2
5.2	5.2	5.2	60.977	534	534	9.14E-18	0.89504	1.1192	0.162467868	13.157	2
7.9	7.9	7.9	37.495	331	331;281	8.22E-12	0.90609	1.1199	0.163369914	9.0644	2
2.4	2.4	2.4	135.58	1217	1217	2.82E-12	0.89601	1.12	0.163498732	6.7028	6
1.5	1.5	1.5	154.59	1318	1318;1312;1173	1.77E-06	0.89358	1.1223	0.166458372	20.866	2
32.8	32.8	32.8	72.421	655	655	8.89E-176	0.92127	1.1229	0.167229454	11.555	33
13.1	13.1	13.1	35.348	320	320;320;251;24	2.01E-13	0.90432	1.1234	0.167871708	5.6816	4
9.2	9.2	9.2	40.746	368	368;325;322;30	5.28E-16	0.88515	1.1251	0.170053235	4.6536	2
9.7	9.7	9.7	49.222	431	431;193	2.71E-16	0.90675	1.1254	0.170437869	51.524	5
13.6	13.6	13.6	20.198	177	177;119	3.59E-06	0.9141	1.1257	0.170822399	2.9537	2
13.2	13.2	13.2	36.908	325	325	2.54E-12	0.95162	1.1259	0.171078696	7.026	4
4.8	4.8	4.8	71.738	660	660;652;652;63	8.37E-12	0.95833	1.1259	0.171078696	20.575	2
9.5	9.5	9.5	114.53	1087	1087;1068;983;'	7.89E-28	0.88614	1.1264	0.171719239	25.011	6
23	23	23	87.819	805	805;780;491;60(	1.21E-113	0.9043	1.1266	0.171975377	6.3942	16
11.2	11.2	11.2	27.566	241	241;200;180	6.19E-09	0.88918	1.1268	0.172231469	6.3241	3
19.2	19.2	19.2	48.141	417	417;214	5.11E-58	0.90733	1.1295	0.175684271	9.0411	7
23.3	23.3	23.3	33.371	309	309;294;293;29	6.95E-30	0.91964	1.1297	0.175939705	3.1962	14
4.2	4.2	4.2	47.628	432	432;392;389;32	4.79E-07	0.87936	1.1298	0.176067406	1.5755	2
6	6	6	30.815	283	283;274	0.00077154	0.88403	1.1305	0.176960992	15.583	2
10.9	10.9	10.9	39.591	366	366;331;288;25	5.08E-16	0.88942	1.1305	0.176960992	3.4151	3
29.3	29.3	29.3	21.525	188	188;172;142;13	1.18E-21	0.91773	1.131	0.177598929	20.834	10
5.4	5.4	5.4	54.416	483	483	2.49E-19	0.90524	1.1327	0.179765808	2.6294	2
3	3	3	532.4	4646	4646	6.61E-27	0.87215	1.1331	0.18027519	7.2411	9
9.4	9.4	9.4	34.482	308	308;256;257	1.61E-09	0.94122	1.1337	0.181038924	14.453	2
10.3	10.3	10.3	37.535	341	341;296;317	4.37E-12	0.89214	1.1339	0.181293413	3.3128	3
14.8	14.8	14.8	134.46	1176	1176;1130;1122	8.06E-70	0.8886	1.1345	0.182056609	6.842	15
1.1	1.1	1.1	129.93	1192	1192;392;373	9.11E-05	0.9483	1.1348	0.182438056	6.5501	2

5.2	5.2	5.2	48.099	442	442	1.77E-09	0.91271	1.1352	0.182946495	6.3246	2
21.4	18.8	18.8	94.33	840	840;148	9.76E-128	0.90941	1.1362	0.184216808	8.2936	21
7.5	7.5	7.5	35.054	321	321;318;318;31	2.50E-05	0.94077	1.1375	0.185866545	0.19773	2
9.1	9.1	9.1	28.48	263	263;160;203	9.99E-09	0.92113	1.1387	0.187387707	37.967	2
11	11	11	86.86	756	756;723;602;80	1.91E-29	0.9166	1.1436	0.193582525	7.1581	7
27.9	27.9	27.9	42.123	390	390;318;314	1.59E-26	0.96818	1.1455	0.195977459	18.95	13
12.9	12.9	12.9	33.777	303	303	8.83E-17	0.91694	1.1456	0.196103398	64.268	3
1.1	1.1	1.1	211.95	1830	1830;336	0.00026239	0.90859	1.1466	0.197362184	4.6939	2
17.6	17.6	17.6	44.868	397	397	5.84E-48	0.89427	1.1477	0.198745582	5.1731	4
16.2	16.2	16.2	37.434	346	346;255	1.18E-10	0.89721	1.1479	0.198996966	11.789	4
24.4	24.4	24.4	41.924	397	397;397	4.38E-54	1.0211	1.1488	0.200127654	6.3372	6
7	7	7	33.631	299	299;258;331	1.54E-08	0.92085	1.1499	0.201508404	15.367	2
8.8	8.8	8.8	28.844	262	262;187;187;11	1.95E-06	0.92986	1.1502	0.201884743	6.9861	2
13.3	13.3	13.3	119.52	1038	1038	8.69E-101	0.90305	1.1529	0.205267382	9.1764	12
11.6	11.6	11.6	23.482	216	216;178;215;21	0.00018203	0.92488	1.1548	0.207643013	8.3704	2
15.2	15.2	15.2	46.836	408	408;361;184;12	5.99E-45	0.90915	1.1558	0.208891775	46.689	4
21.7	21.7	21.7	20.213	184	184;148;120	1.38E-13	0.91084	1.1564	0.209640514	4.0068	3
47.8	40.9	40.9	28.302	247	247;207;233;74	1.43E-162	0.90619	1.1569	0.210264166	26.942	11
3.9	3.9	3.9	83.829	727	727;429;247	5.49E-14	0.92159	1.1574	0.210887549	2.658	3
16.5	16.5	16.5	273.42	2511	2511	1.41E-161	0.91289	1.1578	0.211386062	8.6756	30
9.4	9.4	9.4	46.937	416	416;396;412;27	2.79E-22	0.95281	1.1585	0.212258044	13.37	4
33.6	33.6	33.6	68.741	631	631;623;540;45	3.64E-150	0.94426	1.1608	0.215119425	12.369	34
54.8	54.8	54.8	33.296	299	299;261	1.53E-144	0.9681	1.1611	0.21549223	44.075	27
45.3	45.3	45.3	29.126	254	254;249;239;23	4.52E-121	0.92213	1.1619	0.216485907	10.356	14
11.5	1.7	1.7	71.027	643	643;367	2.26E-67	0.93905	1.1658	0.221320307	5.4957	6
3.2	3.2	3.2	78.365	709	709;694;388	3.85E-09	0.94665	1.1694	0.225768496	2.3967	3
15.5	15.5	15.5	52.164	466	466;308	7.18E-47	0.97065	1.1751	0.232783534	16.271	8
23.2	23.2	23.2	15.521	142	142	1.21E-30	0.91495	1.1775	0.23572706	1.8224	2

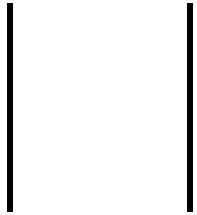
7.9	7.9	7.9	45.594	417	417;345;353;31	3.21E-22	0.93436	1.1798	0.238542314	7.6643	4
6.1	6.1	6.1	34.301	328	328;179;179;10	0.0002603	0.9185	1.1806	0.239520247	6.0047	2
16.7	16.7	16.7	21.995	192	192	7.71E-09	0.9535	1.1816	0.240741731	5.486	3
8.4	8.4	8.4	48.729	453	453;279;451;36	9.25E-20	0.92053	1.1827	0.242084171	6.2334	3
18.3	18.3	18.3	13.802	126	126;126	2.03E-08	0.86851	1.1836	0.243181602	8.625	3
65.6	65.6	65.6	35.936	320	320;319	4.95E-119	0.98566	1.1851	0.2450088	9.0191	30
6.4	6.4	6.4	40.094	362	362;361;361;27	6.95E-08	0.93955	1.1864	0.246590503	4.3346	3
4.6	4.6	4.6	73.46	669	669;598;169;11	4.60E-05	0.95913	1.1891	0.249870047	6.0441	2
15.5	15.5	15.5	30.789	284	284;283	5.18E-09	0.90573	1.1895	0.250355272	9.0087	3
13.1	13.1	13.1	22.284	198	198;180;179;17	0.0011872	0.92551	1.1911	0.252294541	17.858	2
1.1	1.1	1.1	82.577	747	747;72	0.0034238	0.95328	1.1916	0.252900029	12.982	3
17.3	17.3	17.3	39.233	359	359;341;341;31	8.66E-32	0.93758	1.1917	0.253021096	9.8476	9
4.9	4.9	4.9	26.21	243	243;234	1.15E-08	0.93933	1.1925	0.253989266	9.0139	3
10.9	10.9	10.9	68.047	597	597;625;424	9.07E-30	0.99354	1.1926	0.254110242	12.711	7
43.8	43.8	43.8	27.692	256	256;238	2.19E-65	0.95624	1.1932	0.254835883	41.129	16
3.7	3.7	3.7	33.887	298	298;291;286;26	5.48E-05	0.98348	1.195	0.257010618	6.6685	2
10.3	10.3	10.3	23.357	204	204;201;200;19	0.0003744	0.93428	1.1951	0.257131341	1.3296	2
15.8	15.8	15.8	16.937	152	152	1.69E-21	0.91658	1.1958	0.257976116	0.56426	2
19.4	19.4	19.4	48.442	453	453	9.38E-33	0.94251	1.196	0.25821739	58.06	5
15.1	15.1	15.1	32.996	298	298;297	1.09E-16	1.0095	1.1973	0.259784685	14.357	5
13.4	13.4	13.4	30.354	276	276;276;272;25	8.96E-15	0.96438	1.1981	0.260748328	6.6769	3
76.1	76.1	76.1	29.804	272	272;204;201;20	1.22E-191	0.95453	1.2	0.263034406	4.7313	34
22	22	22	12.349	109	109	3.04E-05	0.94725	1.2026	0.266156864	14.181	2
80.9	80.9	80.9	70.289	627	627;246;196;63	0	1.0129	1.2027	0.266276823	18.181	93
10.1	10.1	10.1	53.983	486	486;449	8.51E-19	0.99149	1.2029	0.266516713	18.361	3
39.8	39.8	39.8	59.75	553	553;531;217;16	1.69E-235	0.9576	1.2031	0.266756562	6.1446	35
10.4	10.4	10.4	38.296	357	357;100	1.96E-28	0.92034	1.2035	0.267236142	13.167	2
13.6	10.1	10.1	32.949	286	286;286;174;17	1.49E-26	0.92998	1.2054	0.26951197	15.35	2

61.4	61.4	61.4	56.559	529	529;162;109;13	1.39E-210	0.95845	1.2065	0.270827916	9.4889	64
17	12.5	12.5	30.54	271	271;257;161;23	7.44E-19	0.96732	1.2078	0.272381578	11.746	4
5	5	5	73.243	662	662;660;407;53	1.06E-11	1.019	1.2103	0.275364696	11.684	5
20.8	20.8	20.8	33.331	303	303	1.87E-26	0.96125	1.2107	0.275841423	5.931	7
9.6	9.6	9.6	84.87	760	760;679;81	1.72E-25	0.98383	1.2145	0.28036249	17.077	9
8.6	8.6	8.6	79.685	736	736;761;599	7.84E-47	1.0392	1.2169	0.283210618	9.5744	6
10.6	10.6	10.6	52.645	480	480;222	6.48E-32	0.94849	1.2185	0.285106251	2.8393	4
30.6	30.6	30.6	73.68	679	679;632	9.00E-152	0.99498	1.2211	0.288181352	10.703	38
37.4	37.4	37.4	19.81	174	174;139	4.06E-26	0.95301	1.2229	0.290306435	9.5751	8
2.9	2.9	2.9	147.48	1306	1306;1304;1256	2.95E-13	0.9704	1.2229	0.290306435	8.64	3
7.5	7.5	7.5	37.551	334	334;323;306;25	7.35E-19	0.96245	1.2233	0.290778251	2.6964	2
11.6	11.6	11.6	48.207	430	430;439;431;40	1.22E-16	0.97553	1.2274	0.295605489	5.6542	2
11.3	11.3	11.3	43.383	407	407;378	8.43E-28	0.95205	1.2285	0.296897858	21.52	3
13.8	6.1	0	40.584	362	362;362;362;36	4.56E-53	1.1257	1.2346	0.304043696	2.4749	2
12.2	12.2	12.2	54.177	509	509;486;461	6.82E-35	0.99468	1.2354	0.304978236	4.9212	6
5.5	5.5	5.5	49.966	435	435	4.83E-11	0.9672	1.2367	0.306495572	16.997	2
38.7	38.7	38.7	28.908	256	256;195;100	1.33E-35	1.0043	1.2374	0.307311939	19.419	10
2.8	2.8	2.8	67.454	608	608;235;233	9.99E-05	1.0462	1.2377	0.307661669	6.922	2
36.7	36.7	36.7	16.694	150	150;127	1.78E-15	0.99929	1.2393	0.309525466	10.034	3
60.7	60.7	60.7	35.503	338	338;296;231	4.72E-201	1.0047	1.2424	0.313129735	21.38	51
13.8	13.8	13.8	45.376	399	399;394;305	2.11E-16	1.0997	1.2448	0.315913965	1.8077	5
9.2	6.6	6.6	42.741	379	379	9.80E-12	1.0732	1.2468	0.31823006	19.226	2
49.3	49.3	49.3	23.277	213	213;191;86;74	4.33E-125	1.0001	1.2483	0.319964694	8.8214	12
11.7	11.7	11.7	57.861	529	529;529	4.47E-70	0.98637	1.2501	0.322043506	3.234	6
2.8	2.8	2.8	94.637	831	831;748;739;73	9.58E-07	1.0067	1.2519	0.324119326	33.002	2
44.7	44.7	44.7	18.491	161	161;137;102;16	1.93E-35	1.0159	1.252	0.324234562	2.529	6
12	12	9.3	42.403	376	376;415;405;37	1.06E-21	1.1447	1.2557	0.32849183	12.438	4
32.8	32.8	32.8	77.028	685	685;351;305;26	1.35E-64	1.0019	1.2568	0.329755086	28.143	18

7.4	7.4	7.4	16.561	148	148	0.00033713	1.0126	1.2603	0.333767192	1.98	2
51.5	51.5	51.5	11.367	103	103	1.66E-21	0.95803	1.2625	0.336283388	3.2519	6
17.8	17.8	0	40.976	365	365;371;365;365	8.46E-68	1.1407	1.2665	0.340847077	40.195	4
30	30	8.5	14.095	130	130;130;130;12	2.57E-44	1.0098	1.2697	0.344487663	17.391	8
30	30	30	9.3926	90	90;197;171;130;	1.23E-08	1.0051	1.2729	0.348119084	6.2391	3
23.1	23.1	23.1	54.636	510	510;467	1.76E-79	1.0058	1.2754	0.350949786	4.5281	9
18.2	18.2	18.2	71.502	627	627;592;327;27	3.88E-41	1.0168	1.2781	0.354000719	13.267	13
15.7	15.7	15.7	71.122	661	661;631;630;59	3.71E-36	0.98486	1.2815	0.357833479	26.655	13
46.1	46.1	46.1	20.546	178	178;178;167;99;	2.56E-56	1.0418	1.2838	0.360420466	4.748	9
13.7	13.7	13.7	17.49	168	168	4.52E-14	0.99884	1.2855	0.36232961	4.2279	2
7	7	7	56.5	511	511;513;496;40	1.28E-07	1.0218	1.2872	0.364236231	3.4911	2
7.7	7.7	7.7	57.41	509	509;469;506;46	1.31E-08	1.023	1.2885	0.365692537	8.8601	4
6.9	6.9	6.9	125.14	1145	1145;1101;1091	3.64E-40	1.0099	1.289	0.366252264	3.7716	6
4.6	4.6	4.6	81.069	711	711;708;680	8.48E-16	1.0328	1.2966	0.374733478	19.951	3
10.4	10.4	10.4	27.835	251	251;2063	3.07E-31	1.0355	1.2991	0.377512488	5.0853	4
71.6	71.6	71.6	61.054	573	573;517;448;23	0	1.0739	1.3025	0.381283373	10.082	145
56.5	56.5	56.5	30.772	283	283;184;251;15	1.06E-116	1.0977	1.307	0.386259141	25.901	21
15.4	15.4	15.4	30.886	267	267;254;130;12	3.36E-37	1.0469	1.3072	0.386479889	20.723	7
34.5	34.5	10.6	37.512	330	330;341;427;28	5.48E-97	1.0546	1.3091	0.388575307	7.0471	14
31.2	31.2	31.2	20.694	189	189;97;61	1.47E-37	1.0163	1.3092	0.388685507	11.005	5
55.2	55.2	55.2	11.749	105	105;101;105;10	7.22E-38	1.0346	1.3103	0.389897162	9.3487	7
42.5	42.5	42.5	26.923	261	261;252;169	3.49E-145	1.0568	1.3203	0.400865778	5.06	12
19.9	19.9	19.9	15.388	136	136;136;136;13	5.96E-08	1.0149	1.3241	0.405012083	4.5528	5
4.3	4.3	4.3	94.139	845	845;825;822;35	5.70E-06	1.0752	1.3271	0.408277085	17.833	2
9.5	1.7	0	121.36	1075	1075;1075;952;9	6.56E-147	1.1961	1.3321	0.413702389	3.0499	2
4.2	4.2	4.2	26.049	236	236	3.71E-06	1.0506	1.3322	0.413810687	8.9303	2
29	29	29	19.576	169	169;83	7.70E-15	1.0187	1.3338	0.415542354	2.5003	5
7.3	7.3	7.3	29.38	260	260;227;209;12	2.62E-08	1.1144	1.3358	0.417704019	6.5543	3
17.3	17.3	17.3	31.212	278	278;266;266	6.61E-19	1.0413	1.3411	0.423416817	1.5751	2

54.4	54.4	54.4	104.85	911	911;562;521;41	2.19E-304	1.0673	1.3455	0.428142391	16.85	52
6.4	6.4	6.4	41.389	360	360;316	7.16E-08	1.2041	1.3462	0.428892762	16.104	3
23.3	23.3	23.3	33.515	296	296;232;160	1.16E-91	1.1344	1.3492	0.432104223	9.5182	11
18.3	18.3	18.3	23.264	219	219;219;209;19(	6.53E-16	1.0938	1.3549	0.438186376	3.5421	3
15.5	15.5	15.5	35.619	322	322	1.53E-21	1.1632	1.3621	0.445832624	5.4545	4
32.7	32.7	16.9	30.112	266	266;296;223;26(	2.00E-57	1.0761	1.3662	0.450168697	13.51	17
28	28	23.2	28.607	254	254;254;229;22	2.15E-96	1.0879	1.3669	0.450907702	12.575	20
23.7	23.7	23.7	47.475	430	430;387	2.41E-111	1.1771	1.3676	0.451646328	13.103	12
5	5	5	33.637	320	320;66	2.46E-06	1.1257	1.3733	0.457646819	13.819	2
18.2	18.2	14.7	29.212	258	258;249;228;23	3.61E-24	1.0726	1.3931	0.478298822	3.915	8
32.9	32.9	14.4	32.895	298	298	3.83E-44	1.1479	1.4018	0.487280529	10.125	29
20.1	20.1	20.1	19.856	169	169	3.80E-12	1.1413	1.412	0.497740089	0.73779	2
31.3	35	31.3	18.041	166	166;166;134;12(	1.95E-27	1.0956	1.4188	0.504671235	9.2518	13
12.2	12.2	12.2	26.352	230	230;160;146	3.64E-08	1.1454	1.4203	0.506195692	13.417	2
21.1	21.1	21.1	47.371	418	418;418;348;33(	2.63E-44	1.1183	1.4258	0.511771626	8.869	6
26.7	26.7	26.7	21.588	187	187;181;168;62	7.58E-21	1.1265	1.4301	0.516116031	4.1351	9
4.9	4.9	4.9	35.816	328	328	6.40E-15	1.1803	1.4301	0.516116031	0.8685	2
23.3	23.3	23.3	25.565	227	227	3.56E-35	1.1624	1.4325	0.518535139	5.6563	6
2.4	2.4	2.4	51.146	464	464;378	4.46E-05	1.1399	1.4349	0.520950197	6.61	4
14	14	14	34.333	300	300;165;91;90;3	2.04E-12	1.2287	1.4388	0.524866065	25.3	7
70.7	4.5	4.5	41.792	375	375;356;198;14(	0	1.3186	1.4399	0.525968621	9.602	5
19.2	6.4	0	30.004	266	266	2.16E-28	1.1255	1.4506	0.536649754	1.9281	3
18.1	4.8	4.8	42.003	376	376;197	7.51E-83	1.1777	1.4612	0.547153659	11.616	12
11.4	11.4	11.4	33.077	297	297;130	1.89E-09	1.2558	1.4706	0.55640489	46.343	5
20.8	20.8	20.8	191.61	1675	1675;1639;1640	2.44E-187	1.1747	1.4809	0.566474224	39.972	46
30.2	4.2	4.2	42.051	377	377;377;343;37	2.09E-135	1.2046	1.491	0.576280258	8.1658	18
9.4	9.4	9.4	48.115	417	417;374;177	9.89E-26	1.1695	1.4913	0.576570509	42.565	5
11.2	7.8	7.8	29.357	258	258;249;234;22	1.50E-13	1.1641	1.4983	0.583326519	17.553	2

7.6	7.6	7.6	147.87	1265	1265	1.44E-27	1.1925	1.5065	0.591200673	8.0794	12
19.2	19.2	19.2	57.293	520	520;508;466	9.89E-24	1.2158	1.5153	0.599603448	4.1348	6
34.9	16.4	12.8	32.866	298	298;158	5.51E-41	1.1717	1.5158	0.600079412	10.776	5
6.2	6.2	6.2	26.145	226	226;204;203	1.25E-06	1.1607	1.5243	0.60814687	7.5228	2
12.3	12.3	12.3	125.54	1115	1115;1097;1037	3.93E-50	1.2026	1.5257	0.609471311	5.6358	13
30.6	7.1	7.1	38.518	337	337;323;179;16	3.48E-83	1.2198	1.595	0.673556424	1.8475	2
14.1	9.4	9.4	28.105	255	255;255;255;25	4.91E-20	1.3816	1.6257	0.701061053	1.4116	2
12.6	12.6	12.6	24.722	222	222;222;162;18	5.43E-09	1.3756	1.7051	0.769856352	47.408	2
4.1	4.1	4.1	80.004	724	724;694	6.63E-19	1.6274	2.0293	1.020982161	92.417	2
2.3	2.3	2.3	117.35	1025	1025;1024;1011	1.37E-05	1.6421	2.0624	1.044324169	1.4417	2
8.4	8.4	8.4	65.808	582	582;491;512;18	1.70E-17	1.7856	2.2326	1.158724796	11.054	4
16.1	13.5	13.5	69.948	620	620;600;664;63	2.63E-29	2.2381	2.7073	1.436854764	33.88	8
2.9	2.9	2.9	133.29	1189	1189;1188;976;	9.39E-17	2.6022	3.3223	1.732182353	1.1375	2
47.3	47.3	44.5	66.408	586	586;387	1.93E-197	2.924	3.5242	1.8172958	16.667	47
16.3	16.3	16.3	16.941	153	153	3.55E-18	2.9517	3.7473	1.905851481	131.42	2
12.5	12.5	12.5	31.683	273	273;269;255;23	1.57E-07	4.1493	5.2076	2.380618638	18.391	2
19.1	19.1	19.1	26.119	230	230;229;203;12	5.53E-21	4.5491	5.6357	2.494594816	13.617	8
68.5	68.5	63.3	53.651	466	466;173;470;47	5.88E-210	5.5877	6.9618	2.799460369	71.087	57
24.4	24.4	24.4	72.065	635	635;612;335;76	2.10E-52	8.5982	10.193	3.349506822	34.635	23



Intensity	Intensity L	Intensity H	id	Peptide IDs	Peptide is razor	Mod. peptide ID	Evidence IDs	MS/MS IDs	Best MS/MS	Oxidation (M) si
11371000	11109000	261970	135	3433	TRUE	3592	6098;6099;6100	9156;9157;9158	9157	
5870400	5749400	121040	204	3312;3516;5262	True;True;True;T	3467;3677;5544	5922;6272;9552	8902;9412;1420	8902;9412;14207;14622;14725	
4639800	4499500	140340	377	4496	TRUE	4737	8057;8058	11963;11964	11963	
1880500	1837000	43554	199	1899;3765	True;True	1991;3971	3386;6736	5108;10090	5108;10090	
2406900	2254900	152010	699	224;1199	True;True	233;1261	414;2232;2233	630;3352;3353	630;3353	
2323700	1240700	1083100	848	1071;1819;2779	True;True;True	1128;1909;2908	2013;2014;3274	3015;3016;4936	3016;4937;7453	
5136500	5033200	103270	453	1240;1663;4939	True;True;True;T	1305;1742;5205	2318;2999;8889	3483;4500;1320	3483;4500;13207;13258	
2592800	2460000	132810	647	2945;5113;5409	True;True;True	3087;5386;5700	5251;9237;9810	7909;13729;146	7909;13729;14604	
178260	86502	91762	832	5252;5270	True;True	5533;5552	9539;9566	14185;14231;14	14185;14231	
3219700	2907600	312070	938	414;767;3335;3	True;True;True;T	431;807;3491;4(	782;1460;5959;(	1220;1221;2222	1220;2222;8952	426
4436300	3091900	1344400	239	2548;3425;4046	True;True;True;T	2671;3584;4270	4589;6089;7271	6948;9145;9146	6948;9146;10845;14596	
4431200	2353800	2077400	686	3412;5564	True;True	3571;5865	6071;10112	9119;15052	9119;15052	
1145800	706430	439350	1198	35;2114	True;True	35;2215	52;3767	85;5692	85;5692	
2133500	1494300	639130	1058	110;4488	True;True	111;4728	195;8040	310;11937	310;11937	
1555200	1020400	534800	1148	79;1810;3283	True;True;True	80;1900;3438	141;142;3262;5	227;228;229;49	229;4921;8850	
2561800	1169700	1392100	259	905;3717;4702	True;True;True	949;3917;4953	1690;6634;8402	2566;9951;9952	2566;9952;12477	
9340700	5961800	3378900	841	439;1111;1112;1	True;True;True;T	461;1168;1169;1	825;2063;2064;2	1284;3090;3091	1284;3090;3091	388
13868000	8821700	5046200	773	315;581;2646;3(	True;True;True;T	329;611;2772;3(	566;567;1086;1(	874;875;876;87	877;1661;7189;9859;11301;1130	
11726000	7206600	4519600	298	535;2398;4506;4	True;True;True;T	561;2512;4747;4	1009;4315;8071	1555;1556;6529	1555;6529;11984;12588;13208;1	
2036600	1298900	737660	380	1396;3286;4594	True;True;True	1466;3441;4839	2552;5888;8222	3840;3841;8853	3841;8853;12211	
5150000	3194800	1955300	77	211;3783;3785;3	True;True;True;T	219;3991;3993;3	383;6767;6768;(	583;10140;1014	583;10142;10147;14926	

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21677000	13603000	8073600	1134	962;977;1450;2	True;True;True;T	1013;1030;1523	1795;1796;1836	2713;2714;2715	2714;2776;3956	547;548	
911190	537360	373840	112	174;548	True;True	179;575	325;1032	493;494;1586	493;1586		
9595800	5788500	3807300	745	792;798;1792;1	True;True;True;T	832;838;1881;1	1489;1490;1497	2261;2262;2263	2262;2275;4872;4874;7166;7209		
5420500	3502300	1918200	607	276;1023;1294;4	True;True;True;T	288;1078;1361;4	508;1914;2408;7	779;2879;3621;3	779;2879;3621;11763;14562		
2477200	1515100	962130	104	1881;4058	True;True	1973;4282	3362;3363;7287	5074;5075;1086	5074;10869		
31267000	19222000	12045000	772	313;529;2645;4	True;True;True;T	327;553;2771;4	561;562;563;564	866;867;868;865	869;1528;7185;11300;11442;114		
1447900	947250	500660	646	4668;4883	True;True	4917;5146	8344;8765	12389;13000	12389;13000		
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33167000	20550000	12618000	975	3175;3176;4022	True;True;True;T	3325;3326;4244	5697;5698;7233	8584;8585;8586	8584;8586;1078	446	
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3170300	1817500	1352800	540	160;3224	True;True	164;165;3378	297;298;5806	457;458;459;87	457;8728	262
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75917000	44335000	31582000	1168	968;1604;4303;4	True;True;True;T	1021;1679;4541	1806;2886;2887	2732;4329;4330	2732;4330;11432;13125;13516;1	
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5223700	3163700	2060000	638	1721;2180;2396	True;True;True	1803;2286;2510	3100;3902;3903	4664;4665;5899	4664;5901;6527	
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930790	512360	418420	397	1307;3055	True;True	1374;3203	2422;5495	3642;8291;8292	3642;8292	
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7226300	3735100	3491200	612	1079	TRUE	1136	2022;2023;2024	3031;3032;3033	3034		
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1873500	972720	900790	149	1848;1889	True;True	1939;1981	3315;3373	4998;4999;5089	4999;5089		
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5092900	2685300	2407600	254	1872;1873;2485	False;False;True	1964;1965;2605	3345;3346;3347	5046;5047;5048	5047;5051;6739;9295;10711		
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2558400	1257800	1300600	483	481;2247	True;True	504;2356	900;4004	1396;1397;6056	1396;6056		
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5325700	2671100	2654600	586	2578;4421;4920	True;True;True	2702;4661;5185	4636;4637;4638	7019;7020;7021	7020;11765;13149		
13443000	6630500	6812500	1110	264;1186;1922;:	True;True;True;T	275;1248;2015;:	482;483;2199;2:	740;741;742;32	741;3298;5152;6505;7137;8422;8		
6311500	3144700	3166800	668	614;1270;1678;:	True;True;True;T	644;1335;1758;:	1133;2367;3022	1732;3561;4541	1732;3561;4541	296	
13226000	6432500	6794000	1085	118;119;1826;3	True;True;True;T	120;121;1916;3	224;225;3282;6	342;343;344;49	343;344;4948;9	517	
20698000	10225000	10474000	351	1020;1786;1903	True;True;True;T	1074;1875;1995	1909;3219;3392	2873;4856;4857	2873;4857;5118	193;194	
13447000	6475400	6972000	711	1176;1177;4497	True;True;True;T	1238;1239;4738	2177;2178;2179	3267;3268;3269	3267;3269;11965;15482		
1505800	750910	754890	891	4667;5740	True;True	4916;6046	8343;10427	12387;12388;15	12388;15524		
8148300	3805800	4342500	1100	225;623;624;26	False;False;False	234;654;655;27	415;416;417;41	631;632;633;63	649;1758;1774;7	28	
2820000	1440800	1379200	1145	3050	TRUE	3198	5488;5489	8281;8282;8283	8281		
8555300	4239900	4315400	143	554;801;4232;5	True;True;True;T	582;841;4463;5	1041;1501;1502	1597;2280;2281	1597;2282;1124	82	
3116200	1383600	1732500	425	4639;5065	True;True	4886;5333	8297;9141;9142	12318;13575;13	12318;13575		
7228900	3586300	3642600	1154	1804;5646;5688	True;True;True	1893;5949;5993	3244;10276;103	4891;15296;152	4891;15296;15400		

84070000	40335000	43735000	286	254;288;326;53	True;True;True;T	263;301;302;34	469;526;527;57	717;718;810;81	718;811;894;15	166;167;168;16		
2572600	1138400	1434200	79	2;1958	True;True	2;2052	3;4;3476	6;7;8;9;5245;52	7;5245	49		
16506000	7589500	8916400	776	861;1339;2154;2	True;True;True;T	903;1408;2258;2	1591;1592;1593	2413;2414;2415	2415;3720;5833	339;340		
3277700	1597500	1680200	41	791;5175;5388	True;True;True	831;5452;5679	1488;9379;9777	2259;2260;1394	2260;13945;14551			
3418800	1620300	1798600	197	3696;3916;3963	True;True;True;T	3896;4135;4185	6587;7037;7123	9898;9899;1051	9898;10514;10645;13801			
47418000	21832000	25587000	1186	71;1461;1803;2	True;True;True;T	72;1534;1892;2	121;122;2649;2(	195;196;3985;3	195;3990;4889;5771;11126;1137			
45886000	21697000	24189000	117	435;1439;1506;3	True;True;True;T	457;1512;1580;3	818;819;820;26(	1274;1275;1276	1277;3924;4102	68		
25954000	12127000	13826000	359	517;713;1647;2	True;True;True;T	541;751;1726;2	975;1355;2974;2	1497;1498;2058	1498;2058;4466	198		
1107800	532700	575090	1090	4534	TRUE	4776	8118;8119	12051;12052;12	12052			
17872000	8535800	9335700	1137	591;648;1460;5(	True;True;True;T	621;680;1533;5	1105;1106;1225	1688;1689;1690	1690;1876;3984;15299			
49096000	23025000	26071000	152	84;760;1315;16	True;True;True;T	85;800;1384;17	154;155;156;15	247;248;249;25(	247;2205;3663;4604;5159;8502;1			
2362600	1078000	1284600	598	1368;1385	True;True	1437;1455	2504;2539	3768;3769;3822	3769;3823			
46472000	22004000	24468000	368	425;1348;2660;2	True;True;True;T	444;445;446;14	801;802;803;80	1246;1247;1248	1247;3740;7220	202;203		
4221700	2107600	2114000	187	2129;4901	True;True	2231;5166	3804;8820	5750;13091;130	5750;13092			
16195000	7658700	8536000	556	166;828;953;30(	True;True;True;T	171;869;1004;3	305;1544;1785;5	469;470;2338;2	470;2340;2698;8091;11025;1551			
18573000	8542500	10030000	1116	161;1255;2587;4	True;True;True;T	166;1320;2711;4	299;300;2348;2	460;461;462;46	461;3531;7043;12234;14158			
1158300	530410	627890	245	5166	TRUE	5440	9338;9339	13890;13891	13890			
11671000	5393600	6276900	344	2449;3093;3581	True;True;True;T	2564;3242;3766	4391;4392;5562	6645;6646;6647	6646;8380;9601	186;187;188		
19080000	8784100	10295000	1185	974	TRUE	1027	1829;1830;1831	2765;2766;2767	2768			
5123400	2199400	2924100	115	532;921;2347;3	True;True;True;T	558;971;2459;3	1000;1733;1734	1542;2621;2622	1542;2623;6365;9548			
49015000	20854000	28161000	422	225;623;624;68	False;False;False	234;654;655;71	415;416;417;41	631;632;633;63	649;1758;1774;2	20;21;23;24;25;2		
8649900	3834900	4814900	119	649;1461;1803;2	True;False;False	681;1534;1892;2	1227;1228;2649	1877;1878;1879	1878;3990;4889;5771;10466			
452060000	201770000	250290000	71	682;893;2148;2	False;False;False	717;935;936;22	1276;1277;1636	1954;1955;2479	1955;2481;5795	23;26;27		
2983900	1256400	1727500	166	3542;3601;4416	True;True;True;T	3713;3714;3791	6328;6329;6422	9505;9506;9636	9505;9636;1175	107;108;109		
48165000	21735000	26430000	469	204;338;1302;1	True;True;True;T	210;211;352;13	367;368;369;37	558;559;560;56	559;937;3634;3	235;236		
163700000	72391000	91312000	420	225;623;624;89	False;False;False	234;654;655;93	415;416;417;41	631;632;633;63	649;1758;1774;2	23;25;26;27;213		
5822500	2554200	3268300	405	2932;4097;5674	True;True;True	3074;4322;5977	5233;5234;7368	7879;7880;7881	7879;10977;15360			
3461200	1549100	1912100	1129	870;1460;2136	True;False;True	912;1533;2238	1605;2647;2648	2432;3982;3983	2432;3984;5768			

7008800	3235700	3773100	976	1129;1160;1388	True;True;True;T	1187;1222;1458	2091;2146;2542	3133;3219;3220	3133;3219;3829;4961;11329;125	
4556700	2061100	2495600	179	2333;2905;3221	True;True;True;T	2445;3046;3047	4174;5198;5199	6313;7831;7832	6313;7831;8722;10468;14712;15	
6883100	2804900	4078200	879	85;759;1315;16	True;True;False;	86;799;1384;17	158;1445;1446;2	251;252;2201;2	252;2202;3663;4	406
1585400	617450	967980	90	513	TRUE	537	963;964	1480;1481	1480	
13399000	5960400	7438900	1171	3;555;1534;256	True;True;True;T	3;583;1608;268	5;1042;1043;27	10;11;1598;159	10;1598;4195;6977;8552;8848;92	
3573400	1575200	1998200	126	114;264;1186;19	True;False;False	115;275;1248;2(	199;482;483;21	315;316;740;74	315;741;3298;5152;6505;7137;1(	
915410	376720	538680	1092	1374;1457;5064	True;True;False	1443;1530;5332	2516;2642;9135	3786;3787;3974	3786;3975;13565	
4032300	1411200	2621100	440	307;1720	True;True	321;1802	555;3099	858;4662;4663	858;4662	
1361600	615700	745870	597	468;1124	True;True	490;1182	880;2082	1366;1367;3117	1366;3117	
968820	380350	588470	850	436;3256	True;True	458;3410	821;5853	1278;1279;8805	1278;8805	
2752400	961730	1790700	1059	1979;3214;4017	True;True;True;T	2073;3368;4239	3515;5790;7228	5295;8706;1077	5295;8706;10779;12965	
8818500	2809200	6009300	201	230;343;420;18	True;True;True;T	239;357;437;19	433;621;788;33	663;948;1229;5(	663;948;1229;5038;6845;8402;88	
749500	184420	565090	977	172;4854;5038	True;True;True	177;5115;5306	313;8724;9095	481;12944;1351	481;12944;13510	
94154000	23968000	70186000	781	232;251;421;56	True;True;True;T	241;260;438;59	435;436;437;43	665;666;667;66	666;712;1230;1(	345;346
10850000	1939800	8910700	1041	324;4475	True;True	338;4715	577;8019	891;11906	891;11906	
2005400	355330	1650000	684	12;2361;3969	True;True;True	12;2473;4191	16;4238;7139	28;6415;10664	28;6415;10664	
10152000	1911700	8240100	550	1467;3942;5300	True;True;True;T	1540;4161;4162	2658;7076;7077	4003;10573;105	4003;10574;142	267;268
128030000	23003000	105020000	1046	789;913;1109;1	True;True;True;T	829;959;960;11	1486;1716;1717	2257;2597;2598	2257;2598;3086	484;485;486;487
30058000	3133800	26925000	369	549;1121;1969;2	True;True;True;T	576;577;1179;2(	1033;1034;1035	1587;1588;1589	1590;3112;5263	204;205

Technical replicate of phosphoproteomics experiment in Supplementary Table1: Ptyr network of BCR signalling in JeKo-1 cells following 15 minutes of anti-IgM stimulation Peptides have been sorted basec

Gene name		Protein de	Formula	Protein IDs	Majority p	Peptide co	Peptide co	Peptide co	Fasta head	Proteins	Peptides	Razor + uni	Unique pe	Sequence c	Unique + r	Unique sec
SYK	SYK	SYK Isoforr	Gene_Sym	IPI000185	IPI000185	8;8;4	8;8;4	8;8;4	>IPI:IPI000	3	8	8	8	15.9	15.9	15.9
VIM	VIM	VIM Vimen	Gene_Sym	IPI004184	IPI004184	22;6;3;1;1;	22;6;3;1;1;	20;6;2;0;0;	>IPI:IPI004	13	22	22	20	47.6	47.6	44.2
CD79B	CD79B	CD79B CD7	Gene_Sym	IPI007397	IPI007397	4;4;4;1	4;4;4;1	4;4;4;1	>IPI:IPI007	4	4	4	4	19.1	19.1	19.1
LMNB1	LMNB1	LMNB1 Lar	Gene_Sym	IPI002179	IPI002179	21;19	21;19	21;19	>IPI:IPI002	2	21	21	21	40.1	40.1	40.1
LMNB2	LMNB2	LMNB2 Lar	Gene_Sym	IPI000097	IPI000097	5;5	5;5	5;5	>IPI:IPI000	2	5	5	5	8.2	8.2	8.2
INPP5D	#NAME?	#NAME?	Gene_Sym	IPI003292	IPI003292	2;2;2;1	2;2;2;1	2;2;2;1	>IPI:IPI003	4	2	2	2	1.4	1.4	1.4
HCLS1	HCLS1	HCLS1 Hem	Gene_Sym	IPI000261	IPI000261	2;2	2;2	2;2	>IPI:IPI000	2	2	2	2	4.5	4.5	4.5
COX6C	COX6C	COX6C Cyt	Gene_Sym	IPI000159	IPI000159	2	2	2	>IPI:IPI000	1	2	2	2	20	20	20
UBA2	UBA2	UBA2 SUM	Gene_Sym	IPI000232	IPI000232	2	2	2	>IPI:IPI000	1	2	2	2	2.8	2.8	2.8
FDFT1	FDFT1	FDFT1 Squ	Gene_Sym	IPI000209	IPI000209	1;1	1;1	1;1	>IPI:IPI000	2	1	1	1	4.3	4.3	4.3
HSPE1	HSPE1	HSPE1 10 k	Gene_Sym	IPI002203	IPI002203	4;3;3;1;1;1	4;3;3;1;1;1	4;3;3;1;1;1	>IPI:IPI002	6	4	4	4	45.1	45.1	45.1
HMGCS1	HMGCS1	HMGCS1 H	Gene_Sym	IPI000084	IPI000084	3	3	3	>IPI:IPI000	1	3	3	3	7.7	7.7	7.7
IPO5	IPO5	IPO5 Isofor	Gene_Sym	IPI009393	IPI009393	3;3;2;1;1;1	3;3;2;1;1;1	3;3;2;1;1;1	>IPI:IPI009	15	3	3	3	3.6	3.6	3.6
ACTL6A	ACTL6A	ACTL6A Iso	Gene_Sym	IPI000036	IPI000036	2;2;1;1;1	2;2;1;1;1	2;2;1;1;1	>IPI:IPI000	5	2	2	2	4.9	4.9	4.9
ACTA1	ACTA1	ACTA1 Acti	Gene_Sym	IPI000214	IPI000214	12;12;12;1	1;1;1;1;1;1	1;1;1;1;1;1	>IPI:IPI000	12	12	1	1	31.8	4.2	4.2
CLTC	CLTC	CLTC Isofor	Gene_Sym	IPI000240	IPI000240	11;11;4;4	11;11;4;4	11;11;4;4	>IPI:IPI000	4	11	11	11	8.5	8.5	8.5
ACTBL2	ACTBL2	ACTBL2 Be	Gene_Sym	IPI000032	IPI000032	5	1	1	>IPI:IPI000	1	5	1	1	16.2	4.8	4.8
HIST2H2BF	HIST2H2BF	HIST2H2BF	Gene_Sym	IPI006462	IPI006462	3;3;3;3;3;3	3;3;3;3;3;3	3;3;3;3;3;3	>IPI:IPI006	19	3	3	3	17.5	17.5	17.5
SLC25A5	SLC25A5	SLC25A5 A	Gene_Sym	IPI000071	IPI000071	9	9	2	>IPI:IPI000	1	9	9	2	29.5	29.5	8.1
ACTR3	ACTR3	ACTR3 Acti	Gene_Sym	IPI000280	IPI000280	6;1;1;1;1;1	6;1;1;1;1;1	6;1;1;1;1;1	>IPI:IPI000	8	6	6	6	19.4	19.4	19.4
CYCS	CYCS	CYCS Cyt	Gene_Sym	IPI004653	IPI004653	4;4;3;2;1	4;4;3;2;1	4;4;3;2;1	>IPI:IPI004	5	4	4	4	32.4	32.4	32.4
ACLY	ACLY	ACLY cDNA	Gene_Sym	IPI003948	IPI003948	2;2;2;1	2;2;2;1	2;2;2;1	>IPI:IPI003	4	2	2	2	2.3	2.3	2.3
TTLL3;ARP	TTLL3;ARP	TTLL3;ARP	Gene_Sym	IPI009250	IPI009250	4;4;4;3;3;3	4;4;4;3;3;3	4;4;4;3;3;3	>IPI:IPI009	8	4	4	4	20.3	20.3	20.3
#VALUE!	#VALUE!	HIST2H2A	Gene_Sym	IPI002164	IPI002164	3;3;3;3;3;3	3;3;3;3;3;3	3;3;3;3;3;3	>IPI:IPI002	22	3	3	3	30	30	30
HLA-DPB1	HLA-DPB1	HLA-DPB1	Gene_Sym	IPI008931	IPI008931	3;3;3;2;2;2	3;3;3;2;2;2	2;2;2;1;1;1	>IPI:IPI008	13	3	3	2	14.3	14.3	10.9
#VALUE!	#VALUE!	LOC10013	Gene_Sym	IPI008876	IPI008876	7;5;5	7;5;5	4;4;3	>IPI:IPI008	3	7	7	4	29.7	29.7	16.9
ATP5L	ATP5L	ATP5L ATP	Gene_Sym	IPI000274	IPI000274	3	3	3	>IPI:IPI000	1	3	3	3	32	32	32
FH	FH	FH Isoform	Gene_Sym	IPI002960	IPI002960	4;4	4;4	4;4	>IPI:IPI002	2	4	4	4	10.6	10.6	10.6
CISD2	CISD2	CISD2 CDG	Gene_Sym	IPI001668	IPI001668	2	2	2	>IPI:IPI001	1	2	2	2	14.8	14.8	14.8
#VALUE!	#VALUE!	#VALUE!	Gene_Sym	IPI000051	IPI000051	2;2;2;2;1;1	2;2;2;2;1;1	2;2;2;2;1;1	>IPI:IPI000	24	2	2	2	11.4	11.4	11.4
HARS	HARS	HARS Histi	Gene_Sym	IPI000218	IPI000218	3;3;2;2;2;2	3;3;2;2;2;2	3;3;2;2;2;2	>IPI:IPI000	9	3	3	3	6.1	6.1	6.1
ARPC2	ARPC2	ARPC2 Acti	Gene_Sym	IPI000051	IPI000051	2;1;1	2;1;1	2;1;1	>IPI:IPI000	3	2	2	2	6	6	6

CD74	CD74	CD74 Isofo	CD74 Isofo	Gene_Sym	IPI000229	IPI000229	5;5;3	5;5;3	5;5;3	>IPI:IPI000	3	5	5	5	18.9	18.9	18.9
VDAC1	VDAC1	VDAC1 Vol	VDAC1 Vol	Gene_Sym	IPI002163	IPI002163	9;6;6;5	9;6;6;5	9;6;6;5	>IPI:IPI002	4	9	9	9	45.2	45.2	45.2
UQCRC1	UQCRC1	UQCRC1 C	UQCRC1 C	Gene_Sym	IPI000138	IPI000138	2;1	2;1	2;1	>IPI:IPI000	2	2	2	2	4.6	4.6	4.6
HSPD1	HSPD1	HSPD1 60 k	HSPD1 60 k	Gene_Sym	IPI007841	IPI007841	35;30;16;1	35;30;16;1	35;30;16;1	>IPI:IPI007	11	35	35	35	59.2	59.2	59.2
SFXN1	SFXN1	SFXN1 Side	SFXN1 Side	Gene_Sym	IPI000093	IPI000093	3	3	3	>IPI:IPI000	1	3	3	3	11.8	11.8	11.8
MGC29506	MGC29506	MGC29506	MGC29506	Gene_Sym	IPI001028	IPI001028	2	2	2	>IPI:IPI001	1	2	2	2	11.1	11.1	11.1
ACTN4	ACTN4	ACTN4 Alp	ACTN4 Alp	Gene_Sym	IPI000138	IPI000138	21;14;12;9	21;14;12;9	21;14;12;9	>IPI:IPI000	19	21	21	21	27.3	27.3	27.3
ZNF469	ZNF469	ZNF469 Zin	ZNF469 Zir	Gene_Sym	IPI006446	IPI006446	1	1	1	>IPI:IPI006	1	1	1	1	0.3	0.3	0.3
#VALUE!	#VALUE!	#VALUE!	#VALUE!	#VALUE!	IPI000007	IPI000007	2;2;2;2;1;1	2;2;2;2;1;1	2;2;2;2;1;1	>IPI:IPI000	6	2	2	2	8.7	8.7	8.7
SLC25A6	SLC25A6	SLC25A6 A	SLC25A6 A	Gene_Sym	IPI002914	IPI002914	9;7;2	2;1;0	1;1;0	>IPI:IPI002	3	9	2	1	29.5	8.1	4.4
-	-	cD - cDNA FLJ	- cDNA FLJ	Gene_Sym	IPI006436	IPI006436	3;3;3;3;3;2	2;2;2;2;2;1	2;2;2;2;2;1	>IPI:IPI006	8	3	2	2	11.2	7.8	7.8
PSME3	PSME3	PSME3 Isof	PSME3 Iso	Gene_Sym	IPI002194	IPI002194	3;3;1;1	3;3;1;1	3;3;1;1	>IPI:IPI002	4	3	3	3	15.4	15.4	15.4
PPP1CA	PPP1CA	PPP1CA pr	PPP1CA pr	Gene_Sym	IPI000274	IPI000274	4;4;3;2	4;4;3;2	2;2;1;1	>IPI:IPI000	4	4	4	2	13.2	13.2	5.6
#VALUE!	#VALUE!	#VALUE!	#VALUE!	#VALUE!	IPI004534	IPI004534	4	4	4	>IPI:IPI004	1	4	4	4	38.8	38.8	38.8
THOC6	THOC6	THOC6 Isof	THOC6 Iso	Gene_Sym	IPI003289	IPI003289	2;2;2	2;2;2	2;2;2	>IPI:IPI003	3	2	2	2	7.6	7.6	7.6
EIF2S2	EIF2S2	EIF2S2 Euk	EIF2S2 Euk	Gene_Sym	IPI000217	IPI000217	2;2	2;2	2;2	>IPI:IPI000	2	2	2	2	5.4	5.4	5.4
MCTS1	MCTS1	MCTS1 ma	MCTS1 ma	Gene_Sym	IPI006454	IPI006454	2;2;2	2;2;2	2;2;2	>IPI:IPI006	3	2	2	2	11.5	11.5	11.5
#VALUE!	#VALUE!	HIST2H3D;	HIST2H3D;	Gene_Sym	IPI001716	IPI001716	2;2;2;2;2;2	2;2;2;2;2;2	2;2;2;2;2;2	>IPI:IPI001	13	2	2	2	11.8	11.8	11.8
ATP5C1	ATP5C1	ATP5C1 Isc	ATP5C1 Isc	Gene_Sym	IPI004784	IPI004784	3;2	3;2	3;2	>IPI:IPI004	2	3	3	3	12.1	12.1	12.1
HSD17B10	HSD17B10	HSD17B10	HSD17B10	Gene_Sym	IPI000177	IPI000177	5;4;2	5;4;2	5;4;2	>IPI:IPI000	3	5	5	5	29.1	29.1	29.1
NDUFAF2	NDUFAF2	NDUFAF2 I	NDUFAF2 I	Gene_Sym	IPI000311	IPI000311	2	2	2	>IPI:IPI000	1	2	2	2	20.1	20.1	20.1
HADH	HADH	HADH Isofo	HADH Isofo	Gene_Sym	IPI002984	IPI002984	3;3;3	3;3;3	3;3;3	>IPI:IPI002	3	3	3	3	7.7	7.7	7.7
HSPA9	HSPA9	HSPA9 Stre	HSPA9 Stre	Gene_Sym	IPI000077	IPI000077	14;8	14;8	14;8	>IPI:IPI000	2	14	14	14	27.4	27.4	27.4
CANX	CANX	CANX cDNA	CANX cDN	Gene_Sym	IPI000209	IPI000209	7;7;3;2;2	7;7;3;2;2	7;7;3;2;2	>IPI:IPI000	5	7	7	7	11.6	11.6	11.6
ARPC3	ARPC3	ARPC3 Acti	ARPC3 Acti	Gene_Sym	IPI000051	IPI000051	2;2;2;1;1	2;2;2;1;1	2;2;2;1;1	>IPI:IPI000	5	2	2	2	11.2	11.2	11.2
UQCRC2	UQCRC2	UQCRC2 C	UQCRC2 C	Gene_Sym	IPI003053	IPI003053	3	3	3	>IPI:IPI003	1	3	3	3	10.6	10.6	10.6
ATP5O	ATP5O	ATP5O ATP	ATP5O ATP	Gene_Sym	IPI000076	IPI000076	5;2;2;1	5;2;2;1	5;2;2;1	>IPI:IPI000	4	5	5	5	31.9	31.9	31.9
ATP5B	ATP5B	ATP5B ATP	ATP5B ATP	Gene_Sym	IPI003034	IPI003034	16;6;4;2;1;	16;6;4;2;1;	16;6;4;2;1;	>IPI:IPI003	6	16	16	16	38	38	38
#VALUE!	#VALUE!	LOC10013	LOC10013	Gene_Sym	IPI009369	IPI009369	3;3;3	3;3;3	3;3;3	>IPI:IPI009	3	3	3	3	17.6	17.6	17.6
#VALUE!	#VALUE!	SLC3A2;LO	SLC3A2;LO	Gene_Sym	IPI005544	IPI005544	4;4;4;4;4;4	4;4;4;4;4;4	4;4;4;4;4;4	>IPI:IPI005	7	4	4	4	7.4	7.4	7.4
TFRC	TFRC	TFRC Trans	TFRC Trans	Gene_Sym	IPI000224	IPI000224	2;2	2;2	2;2	>IPI:IPI000	2	2	2	2	2.9	2.9	2.9
LOC64604	LOC64604	LOC64604	LOC64604	Gene_Sym	IPI008869	IPI008869	2;2	2;2	2;2	>IPI:IPI008	2	2	2	2	2.6	2.6	2.6
#VALUE!	#VALUE!	UBB;UBC;R	UBB;UBC;F	Gene_Sym	IPI007981	IPI007981	3;3;3;3;3;3	3;3;3;3;3;3	3;3;3;3;3;3	>IPI:IPI007	23	3	3	3	44.7	44.7	44.7
ATP5H	ATP5H	ATP5H Isof	ATP5H Isof	Gene_Sym	IPI002204	IPI002204	4;4;4;1;1	4;4;4;1;1	4;4;4;1;1	>IPI:IPI002	5	4	4	4	31.7	31.7	31.7
DCI	DCI	DCI Isoforn	DCI Isoforr	Gene_Sym	IPI003005	IPI003005	3;3	3;3	3;3	>IPI:IPI003	2	3	3	3	10.3	10.3	10.3
#VALUE!	#VALUE!	#VALUE!	#VALUE!	#VALUE!	IPI006548	IPI006548	1	1	1	>IPI:IPI006	1	1	1	1	4.2	4.2	4.2
EEF1E1	EEF1E1	EEF1E1 Eul	EEF1E1 Eul	Gene_Sym	IPI000035	IPI000035	1;1	1;1	1;1	>IPI:IPI000	2	1	1	1	5.7	5.7	5.7
MDH2	MDH2	MDH2 Mal	MDH2 Mal	Gene_Sym	IPI002910	IPI002910	15;12;11	15;12;11	15;12;11	>IPI:IPI002	3	15	15	15	55.3	55.3	55.3
NARG1	NARG1	NARG1 Isof	NARG1 Iso	Gene_Sym	IPI003861	IPI003861	2;2	2;2	2;2	>IPI:IPI003	2	2	2	2	2.2	2.2	2.2
SPCS3	SPCS3	SPCS3 Sign	SPCS3 Sign	Gene_Sym	IPI003002	IPI003002	3	3	3	>IPI:IPI003	1	3	3	3	17.8	17.8	17.8
ATP5A1	ATP5A1	ATP5A1 AT	ATP5A1 AT	Gene_Sym	IPI004404	IPI004404	17;14;9;8;6	17;14;9;8;6	17;14;9;8;6	>IPI:IPI004	5	17	17	17	35.8	35.8	35.8

LCP1	LCP1	LCP1 Plasti	LCP1 Plasti	Gene_Sym	IPI0001047	IPI0001047	33;9;7;5;5;	33;9;7;5;5;	33;9;7;5;5;	>IPI:IPI000	10	33	33	33	61.7	61.7	61.7
APEH	APEH	APEH Putat	APEH Puta	Gene_Sym	IPI0092664	IPI0092664	2;2;2;2;1;1	2;2;2;2;1;1	2;2;2;2;1;1	>IPI:IPI009	6	2	2	2	3.1	3.1	3.1
TMEM109	TMEM109	TMEM109	TMEM109	Gene_Sym	IPI0003169	IPI0003169	1;1	1;1	1;1	>IPI:IPI000	2	1	1	1	4.9	4.9	4.9
APRT	APRT	APRT Aden	APRT Ader	Gene_Sym	IPI0021869	IPI0021869	5;5;1	5;5;1	5;5;1	>IPI:IPI002	3	5	5	5	28.3	28.3	28.3
ANXA5	ANXA5	ANXA5 Anr	ANXA5 Ani	Gene_Sym	IPI0032980	IPI0032980	13;13	13;13	13;13	>IPI:IPI003	2	13	13	13	40.3	40.3	40.3
ATP5F1	ATP5F1	ATP5F1 AT	ATP5F1 AT	Gene_Sym	IPI0002913	IPI0002913	4;3;2	4;3;2	4;3;2	>IPI:IPI000	3	4	4	4	15.2	15.2	15.2
MAT2A	MAT2A	MAT2A S-a	MAT2A S-a	Gene_Sym	IPI0001015	IPI0001015	2;2	2;2	2;2	>IPI:IPI000	2	2	2	2	7.6	7.6	7.6
HSD17B4	HSD17B4	HSD17B4 P	HSD17B4 F	Gene_Sym	IPI0001991	IPI0001991	3;1	3;1	3;1	>IPI:IPI000	2	3	3	3	4.6	4.6	4.6
HSPA5	HSPA5	HSPA5 HSP	HSPA5 HSF	Gene_Sym	IPI0000336	IPI0000336	16	15	15	>IPI:IPI000	1	16	15	15	26.3	26.3	26.3
PHB	PHB	PHB Prohit	PHB Prohit	Gene_Sym	IPI0001733	IPI0001733	11;7;7;6;4;	11;7;7;6;4;	11;7;7;6;4;	>IPI:IPI000	7	11	11	11	49.6	49.6	49.6
G3BP1	G3BP1	G3BP1 Ras	G3BP1 Ras	Gene_Sym	IPI0001244	IPI0001244	4;2	4;2	4;2	>IPI:IPI000	2	4	4	4	12	12	12
PDCD6IP	PDCD6IP	PDCD6IP p	PDCD6IP p	Gene_Sym	IPI0093807	IPI0093807	4;4	4;4	4;4	>IPI:IPI009	2	4	4	4	5.5	5.5	5.5
SSB	SSB	SSB Lupus	SSB Lupus	Gene_Sym	IPI0000903	IPI0000903	2;2;1;1	2;2;1;1	2;2;1;1	>IPI:IPI000	4	2	2	2	6.1	6.1	6.1
SEC11A	SEC11A	SEC11A Sig	SEC11A Sig	Gene_Sym	IPI0087360	IPI0087360	2;2;2;2	2;2;2;2	2;2;2;2	>IPI:IPI008	4	2	2	2	9	9	9
PSMB8	PSMB8	PSMB8 Isof	PSMB8 Iso	Gene_Sym	IPI0000078	IPI0000078	3;3;3;2;2;1	3;3;3;2;2;1	3;3;3;2;2;1	>IPI:IPI000	6	3	3	3	13.4	13.4	13.4
PSME2	PSME2	PSME2 Put	PSME2 Put	Gene_Sym	IPI0094318	IPI0094318	7;7;7;3	7;7;7;3	7;7;7;3	>IPI:IPI009	4	7	7	7	41.7	41.7	41.7
SOD2	SOD2	SOD2 Supe	SOD2 Supe	Gene_Sym	IPI0002231	IPI0002231	2;2;2;1	2;2;2;1	2;2;2;1	>IPI:IPI000	4	2	2	2	12.6	12.6	12.6
TKT	TKT	TKT cDNA I	TKT cDNA I	Gene_Sym	IPI0064392	IPI0064392	15;15;14;1	15;15;14;1	15;15;14;1	>IPI:IPI006	9	15	15	15	31.4	31.4	31.4
PRDX3	PRDX3	PRDX3 Thic	PRDX3 Thi	Gene_Sym	IPI0002491	IPI0002491	8;8	8;8	8;8	>IPI:IPI000	2	8	8	8	37.1	37.1	37.1
FASN	FASN	FASN Fatty	FASN Fatty	Gene_Sym	IPI0002678	IPI0002678	13	13	13	>IPI:IPI000	1	13	13	13	6.4	6.4	6.4
GLUD1	GLUD1	GLUD1 Glu	GLUD1 Glu	Gene_Sym	IPI0001680	IPI0001680	3;3	3;3	3;3	>IPI:IPI000	2	3	3	3	4.7	4.7	4.7
IARS	IARS	IARS Isoleu	IARS Isoleu	Gene_Sym	IPI0064412	IPI0064412	3;3	3;3	3;3	>IPI:IPI006	2	3	3	3	2.1	2.1	2.1
HSPA4	HSPA4	HSPA4	HSPA4	Gene_Sym	IPI0000296	IPI0000296	9;3	7;3	7;3	>IPI:IPI000	2	9	7	7	14.9	12.3	12.3
CALR	CALR	CALR Calre	CALR Calre	Gene_Sym	IPI0002059	IPI0002059	2;1	2;1	2;1	>IPI:IPI000	2	2	2	2	6.2	6.2	6.2
SERPINB9	SERPINB9	SERPINB9 S	SERPINB9 S	Gene_Sym	IPI0003213	IPI0003213	5	5	5	>IPI:IPI000	1	5	5	5	14.9	14.9	14.9
AK2	AK2	AK2 Isoforr	AK2 Isoforr	Gene_Sym	IPI0021590	IPI0021590	5;5;5;4;3;2	5;5;5;4;3;2	5;5;5;4;3;2	>IPI:IPI002	6	5	5	5	26.4	26.4	26.4
ACO2	ACO2	ACO2 Acor	ACO2 Acor	Gene_Sym	IPI0079073	IPI0079073	9;9;7;4	9;9;7;4	9;9;7;4	>IPI:IPI007	4	9	9	9	14.4	14.4	14.4
TBCA	TBCA	TBCA Tubu	TBCA Tubu	Gene_Sym	IPI0021723	IPI0021723	5;3	5;3	5;3	>IPI:IPI002	2	5	5	5	44.4	44.4	44.4
UBE2D3	UBE2D3	UBE2D3 Isc	UBE2D3 Isc	Gene_Sym	IPI0037514	IPI0037514	2;2;2;2;1;1	2;2;2;2;1;1	2;2;2;2;1;1	>IPI:IPI003	7	2	2	2	12.1	12.1	12.1
LARS	LARS	LARS Leucy	LARS Leucy	Gene_Sym	IPI0010395	IPI0010395	6;6;5;1	6;6;5;1	6;6;5;1	>IPI:IPI001	4	6	6	6	5.4	5.4	5.4
ALOX5AP	ALOX5AP	ALOX5AP A	ALOX5AP A	Gene_Sym	IPI0002297	IPI0002297	3	3	3	>IPI:IPI000	1	3	3	3	17.4	17.4	17.4
RCSD1	RCSD1	RCSD1 Isof	RCSD1 Isof	Gene_Sym	IPI0001765	IPI0001765	2;2	2;2	2;2	>IPI:IPI000	2	2	2	2	6.5	6.5	6.5
AARS	AARS	AARS cDNA	AARS cDNA	Gene_Sym	IPI0091070	IPI0091070	6;6	6;6	6;6	>IPI:IPI009	2	6	6	6	6.4	6.4	6.4
DLSTP;DLS	DLSTP;DLS	DLSTP;DLS	DLSTP;DLS	Gene_Sym	IPI0042010	IPI0042010	5;4;3;2;1	5;4;3;2;1	5;4;3;2;1	>IPI:IPI004	5	5	5	5	14.3	14.3	14.3
XPOT	XPOT	XPOT Expo	XPOT Expo	Gene_Sym	IPI0030629	IPI0030629	2	2	2	>IPI:IPI003	1	2	2	2	2.7	2.7	2.7
SGTA	SGTA	SGTA Smal	SGTA Smal	Gene_Sym	IPI0001394	IPI0001394	3;2	3;2	3;2	>IPI:IPI000	2	3	3	3	12.1	12.1	12.1
PHB2	PHB2	PHB2 Proh	PHB2 Proh	Gene_Sym	IPI0002725	IPI0002725	12;10	12;10	12;10	>IPI:IPI000	2	12	12	12	45.2	45.2	45.2
PDIA3	PDIA3	PDIA3 Prot	PDIA3 Prot	Gene_Sym	IPI0002525	IPI0002525	6;3;2;1	6;3;2;1	4;2;0;1	>IPI:IPI000	4	6	6	4	14.3	14.3	10.1
IPO7	IPO7	IPO7 Impo	IPO7 Impo	Gene_Sym	IPI0000740	IPI0000740	5	5	5	>IPI:IPI000	1	5	5	5	6	6	6
UCHL3	UCHL3	UCHL3 Ubi	UCHL3 Ubi	Gene_Sym	IPI0001125	IPI0001125	2;1	2;1	2;1	>IPI:IPI000	2	2	2	2	10.9	10.9	10.9
HSP90B1	HSP90B1	HSP90B1 E	HSP90B1 E	Gene_Sym	IPI0002723	IPI0002723	14;7;5;1	12;7;3;1	12;7;3;1	>IPI:IPI000	4	14	12	12	19.2	17.4	17.4

RARS	RARS	RARS Isofo	RARS Isofo	Gene_Sym	IPI000048(	IPI000048(	3;3	3;3	3;3	>IPI:IPI000	2	3	3	3	5.5	5.5	5.5
KPNB1	KPNB1	KPNB1 Imp	KPNB1 Imp	Gene_Sym	IPI000016:	IPI000016:	9;4	9;4	9;4	>IPI:IPI000	2	9	9	9	12.6	12.6	12.6
VDAC2	VDAC2	VDAC2 Isof	VDAC2 Isof	Gene_Sym	IPI009025(	IPI009025(	8;8;8;8;8;8	8;8;8;8;8;8	8;8;8;8;8;8	>IPI:IPI009	10	8	8	8	30.7	30.7	30.7
DLAT	DLAT	DLAT Dihyc	DLAT Dihyc	Gene_Sym	IPI000213:	IPI000213:	5;4	5;4	5;4	>IPI:IPI000	2	5	5	5	7.4	7.4	7.4
IDH3A	IDH3A	IDH3A Isof	IDH3A Isof	Gene_Sym	IPI000307(	IPI000307(	4;4;2;2	4;4;2;2	4;4;2;2	>IPI:IPI000	4	4	4	4	11.2	11.2	11.2
PSME1	PSME1	PSME1 Pro	PSME1 Prc	Gene_Sym	IPI0047972	IPI0047972	7;6	7;6	7;6	>IPI:IPI004	2	7	7	7	27.3	27.3	27.3
DARS	DARS	DARS Aspa	DARS Aspa	Gene_Sym	IPI002169:	IPI002169:	3;2;2;2;2;1	3;2;2;2;2;1	3;2;2;2;2;1	>IPI:IPI002	6	3	3	3	5.8	5.8	5.8
TIMM50	TIMM50	TIMM50 Is	TIMM50 Is	Gene_Sym	IPI004184:	IPI004184:	2;2	2;2	2;2	>IPI:IPI004	2	2	2	2	5.9	5.9	5.9
KARS	KARS	KARS Isofo	KARS Isofo	Gene_Sym	IPI003070:	IPI003070:	3;3;1	3;3;1	3;3;1	>IPI:IPI003	3	3	3	3	6.4	6.4	6.4
LRRC59	LRRC59	LRRC59 Le	LRRC59 Le	Gene_Sym	IPI003963:	IPI003963:	2	2	2	>IPI:IPI003	1	2	2	2	7.2	7.2	7.2
CAPZA1	CAPZA1	CAPZA1 F-a	CAPZA1 F-a	Gene_Sym	IPI000059(	IPI000059(	4;4;1;1;1	4;4;1;1;1	3;3;0;0;0	>IPI:IPI000	5	4	4	3	19.6	19.6	16.1
EPRS	EPRS	EPRS Bifun	EPRS Bifun	Gene_Sym	IPI000134:	IPI000134:	5;4	5;4	5;4	>IPI:IPI000	2	5	5	5	3.2	3.2	3.2
SUB1	SUB1	SUB1 Activ	SUB1 Activ	Gene_Sym	IPI002212:	IPI002212:	2;1	2;1	2;1	>IPI:IPI002	2	2	2	2	18.9	18.9	18.9
DBNL	DBNL	DBNL Isofo	DBNL Isofo	Gene_Sym	IPI001019(	IPI001019(	2;2;2;2;2;1	2;2;2;2;2;1	2;2;2;2;2;1	>IPI:IPI001	16	2	2	2	6.2	6.2	6.2
CAPRIN1	CAPRIN1	CAPRIN1 Is	CAPRIN1 Is	Gene_Sym	IPI0078387	IPI0078387	2;2;2	2;2;2	2;2;2	>IPI:IPI007	3	2	2	2	3.2	3.2	3.2
LASP1	LASP1	LASP1 Isof	LASP1 Isof	Gene_Sym	IPI003868(	IPI003868(	2;2;2;2;1;1	2;2;2;2;1;1	2;2;2;2;1;1	>IPI:IPI003	7	2	2	2	5.9	5.9	5.9
NME1	NME1	NME1 Isof	NME1 Isof	Gene_Sym	IPI003755:	IPI003755:	8;8;3	1;1;1	1;1;1	>IPI:IPI003	3	8	1	1	45.8	7.9	7.9
NDUFS3	NDUFS3	NDUFS3 N/	NDUFS3 N/	Gene_Sym	IPI000257:	IPI000257:	4	4	4	>IPI:IPI000	1	4	4	4	22	22	22
RPS15A	RPS15A	RPS15A 40	RPS15A 40	Gene_Sym	IPI002210:	IPI002210:	4;2;1	4;2;1	4;2;1	>IPI:IPI002	3	4	4	4	27.7	27.7	27.7
IMPDH2	IMPDH2	IMPDH2 In	IMPDH2 In	Gene_Sym	IPI002915:	IPI002915:	8;8;5;5;5;1	8;8;5;5;5;1	8;8;5;5;5;1	>IPI:IPI002	16	8	8	8	20	20	20
#VALUE!	#VALUE!			Gene_Sym	IPI002195:	IPI002195:	3;2;2;1	3;2;2;1	3;2;2;1	>IPI:IPI002	4	3	3	3	3.9	3.9	3.9
C14orf156	C14orf156	C14orf156	C14orf156	Gene_Sym	IPI000099:	IPI000099:	1	1	1	>IPI:IPI000	1	1	1	1	9.2	9.2	9.2
YWHAG	YWHAG	YWHAG 14	YWHAG 14	Gene_Sym	IPI002206:	IPI002206:	7;6	4;3	4;3	>IPI:IPI002	2	7	4	4	35.2	21.5	21.5
#VALUE!	#VALUE!	#VALUE!	#VALUE!	#VALUE!	IPI000213:	IPI000213:	5;4;4;1	5;4;4;1	5;4;4;1	>IPI:IPI000	4	5	5	5	23	23	23
RANP1;RAI	RANP1;RAI	RANP1;RAI	RANP1;RAI	Gene_Sym	IPI007923:	IPI007923:	7;7;7;7;3;3	7;7;7;7;3;3	7;7;7;7;3;3	>IPI:IPI007	6	7	7	7	28.8	28.8	28.8
NAMPT	NAMPT	NAMPT Nic	NAMPT Nic	Gene_Sym	IPI000188:	IPI000188:	2;2;1;1	2;2;1;1	2;2;1;1	>IPI:IPI000	4	2	2	2	3.9	3.9	3.9
COTL1	COTL1	COTL1 Coa	COTL1 Coa	Gene_Sym	IPI000177(	IPI000177(	3	3	3	>IPI:IPI000	1	3	3	3	16.2	16.2	16.2
PSMB1	PSMB1	PSMB1 Pro	PSMB1 Prc	Gene_Sym	IPI000250:	IPI000250:	3;1	3;1	3;1	>IPI:IPI000	2	3	3	3	17.8	17.8	17.8
GNB2	GNB2	GNB2 Gua	GNB2 Gua	Gene_Sym	IPI000033-	IPI000033-	2;2;2;2;2;2	2;2;2;2;2;2	2;2;2;2;2;2	>IPI:IPI000	13	2	2	2	6.2	6.2	6.2
NPEPPS	NPEPPS	NPEPPS Pu	NPEPPS Pu	Gene_Sym	IPI000262:	IPI000262:	6;2;2	6;2;2	6;2;2	>IPI:IPI000	3	6	6	6	7.2	7.2	7.2
HSP90AA1	HSP90AA1	HSP90AA1	HSP90AA1	Gene_Sym	IPI003824:	IPI003824:	27;27;16;6	13;13;10;1	13;13;10;1	>IPI:IPI003	6	27	13	13	28.8	15.6	15.6
SYNE1	SYNE1	SYNE1 Isof	SYNE1 Isof	Gene_Sym	IPI003864-	IPI003864-	2;2;2;2;2;1	2;2;2;2;2;1	2;2;2;2;2;1	>IPI:IPI003	9	2	2	2	0.2	0.2	0.2
PSMA6	PSMA6	PSMA6 Pro	PSMA6 Prc	Gene_Sym	IPI000296:	IPI000296:	5;3;1	5;3;1	5;3;1	>IPI:IPI000	3	5	5	5	25.2	25.2	25.2
#VALUE!	#VALUE!	DDB1;LOC:	DDB1;LOC:	Gene_Sym	IPI002934(	IPI002934(	2;2;2;1	2;2;2;1	2;2;2;1	>IPI:IPI002	4	2	2	2	1.6	1.6	1.6
PGAM5;PX	PGAM5;PX	PGAM5;PX	PGAM5;PX	Gene_Sym	IPI007889(	IPI007889(	1;1;1;1	1;1;1;1	1;1;1;1	>IPI:IPI007	4	1	1	1	3.5	3.5	3.5
#VALUE!	#VALUE!	#VALUE!	#VALUE!	#VALUE!	IPI007959(	IPI007959(	3;3;3;3;3;3	3;3;3;3;3;3	1;1;1;1;1;1	>IPI:IPI007	566	3	3	1	9	9	3.3
RPL27	RPL27	RPL27 60S	RPL27 60S	Gene_Sym	IPI002191:	IPI002191:	2;1;1	2;1;1	2;1;1	>IPI:IPI002	3	2	2	2	12.5	12.5	12.5
YBX1	YBX1	YBX1 Nucle	YBX1 Nucle	Gene_Sym	IPI000318(	IPI000318(	3;3;2;2;2;1	3;3;2;2;2;1	1;1;1;0;1;0	>IPI:IPI000	8	3	3	1	13.6	13.6	5.9
EIF3F	EIF3F	EIF3F HCG:	EIF3F HCG:	Gene_Sym	IPI006547:	IPI006547:	7;7	7;7	7;7	>IPI:IPI006	2	7	7	7	26.6	26.6	26.6
CCT6A	CCT6A	CCT6A T-cc	CCT6A T-cc	Gene_Sym	IPI0002762	IPI0002762	8;7;3;2;1	8;7;3;2;1	8;7;3;2;1	>IPI:IPI000	5	8	8	8	19	19	19
HSPA6	HSPA6	HSPA6 Hea	HSPA6 Hea	Gene_Sym	IPI003926(	IPI003926(	6;3	1;1	1;1	>IPI:IPI003	2	6	1	1	11.5	1.7	1.7

GSTO1	GSTO1	GSTO1 Glu	GSTO1 Glu	Gene_Sym	IPI000197	IPI000197	3;2;1	3;2;1	3;2;1	>IPI:IPI000	3	3	3	3	13.7	13.7	13.7
TCL1A	TCL1A	TCL1A T-ce	TCL1A T-ce	Gene_Sym	IPI001787	IPI001787	2	2	2	>IPI:IPI001	1	2	2	2	13.2	13.2	13.2
NASP	NASP	NASP Isofo	NASP Isofo	Gene_Sym	IPI003324	IPI003324	2;2;2;2	2;2;2;2	2;2;2;2	>IPI:IPI003	4	2	2	2	2.3	2.3	2.3
RPL30	RPL30	RPL30 60S	RPL30 60S	Gene_Sym	IPI002191	IPI002191	2;2;1;1;1	2;2;1;1;1	2;2;1;1;1	>IPI:IPI002	5	2	2	2	24.3	24.3	24.3
PDCD6	PDCD6	PDCD6 Pro	PDCD6 Pro	Gene_Sym	IPI000252	IPI000252	3;3;3	3;3;3	3;3;3	>IPI:IPI000	3	3	3	3	17.8	17.8	17.8
PMVK	PMVK	PMVK Pho	PMVK Pho	Gene_Sym	IPI002206	IPI002206	3	3	3	>IPI:IPI002	1	3	3	3	14.1	14.1	14.1
NME2;NM	NME2;NMI	NME2;NMI	NME2;NM	Gene_Sym	IPI006045	IPI006045	10;10;8;5;5	10;10;8;5;5	3;3;3;3;0;2	>IPI:IPI006	8	10	10	3	49	49	9.9
BPNT1	BPNT1	BPNT1 Isof	BPNT1 Isof	Gene_Sym	IPI004102	IPI004102	3;3;3;3	3;3;3;3	3;3;3;3	>IPI:IPI004	4	3	3	3	9.5	9.5	9.5
#VALUE!	#VALUE!	#VALUE!	#VALUE!	#VALUE!	IPI006454	IPI006454	2;2;2;2;2;2	2;2;2;2;2;2	2;2;2;2;2;2	>IPI:IPI006	11	2	2	2	2.2	2.2	2.2
TUBB2C	TUBB2C	TUBB2C Tu	TUBB2C Tu	Gene_Sym	IPI000077	IPI000077	19;15;9;9;8	4;3;1;2;1;1	1;1;0;0;0;0	>IPI:IPI000	12	19	4	1	55.3	13.3	2.7
TCP1	TCP1	TCP1 T-con	TCP1 T-cor	Gene_Sym	IPI002905	IPI002905	5;4	5;4	5;4	>IPI:IPI002	2	5	5	5	11.7	11.7	11.7
ETFB	ETFB	ETFB Isofo	ETFB Isofo	Gene_Sym	IPI005564	IPI005564	3;3	3;3	3;3	>IPI:IPI005	2	3	3	3	9.2	9.2	9.2
CAND1	CAND1	CAND1 Iso	CAND1 Iso	Gene_Sym	IPI001001	IPI001001	5;4;1	5;4;1	5;4;1	>IPI:IPI001	3	5	5	5	5	5	5
RPS11	RPS11	RPS11 40S	RPS11 40S	Gene_Sym	IPI000250	IPI000250	5;2	5;2	5;2	>IPI:IPI000	2	5	5	5	34.2	34.2	34.2
GSTP1	GSTP1	GSTP1 Glut	GSTP1 Glu	Gene_Sym	IPI002197	IPI002197	9;6;1	9;6;1	9;6;1	>IPI:IPI002	3	9	9	9	52.4	52.4	52.4
PSMA2	PSMA2	PSMA2 Pro	PSMA2 Pro	Gene_Sym	IPI002196	IPI002196	4;2;2;1	4;2;2;1	4;2;2;1	>IPI:IPI002	4	4	4	4	29.9	29.9	29.9
TRAP1	TRAP1	TRAP1 Hea	TRAP1 Hea	Gene_Sym	IPI000302	IPI000302	2;1	2;1	2;1	>IPI:IPI000	2	2	2	2	3.6	3.6	3.6
CAPZB	CAPZB	CAPZB cDN	CAPZB cDN	Gene_Sym	IPI002187	IPI002187	7;7;5;2;2;2	7;7;5;2;2;2	7;7;5;2;2;2	>IPI:IPI002	6	7	7	7	15.2	15.2	15.2
PDHB	PDHB	PDHB Isofo	PDHB Isofo	Gene_Sym	IPI000039	IPI000039	2;2;2;2;2;2	2;2;2;2;2;2	2;2;2;2;2;2	>IPI:IPI000	7	2	2	2	5.3	5.3	5.3
UBE2V2	UBE2V2	UBE2V2 Ub	UBE2V2 Ub	Gene_Sym	IPI000196	IPI000196	4;3;2;2	4;3;2;2	2;1;1;0	>IPI:IPI000	4	4	4	2	26.9	26.9	14.5
SH3BGRL	SH3BGRL	SH3BGRL S	SH3BGRL S	Gene_Sym	IPI000253	IPI000253	3	3	3	>IPI:IPI000	1	3	3	3	30.7	30.7	30.7
RPL18A	RPL18A	RPL18A 60	RPL18A 60	Gene_Sym	IPI000262	IPI000262	3;3;2;2	3;3;2;2	3;3;2;2	>IPI:IPI000	4	3	3	3	16.5	16.5	16.5
TCEA1	TCEA1	TCEA1 Isof	TCEA1 Isof	Gene_Sym	IPI003332	IPI003332	2;2;2;1;1	2;2;2;1;1	2;2;2;1;1	>IPI:IPI003	5	2	2	2	6.3	6.3	6.3
ARF1	ARF1	ARF1 ADP-I	ARF1 ADP-	Gene_Sym	IPI002159	IPI002159	2;2;2;1;1;1	2;2;2;1;1;1	1;1;1;1;1;0	>IPI:IPI002	6	2	2	1	13.3	13.3	7.7
ETFA	ETFA	ETFA Electr	ETFA Electr	Gene_Sym	IPI000108	IPI000108	4;4;3	4;4;3	4;4;3	>IPI:IPI000	3	4	4	4	16.5	16.5	16.5
RPS13	RPS13	RPS13 40S	RPS13 40S	Gene_Sym	IPI002210	IPI002210	3	3	3	>IPI:IPI002	1	3	3	3	19.2	19.2	19.2
PSMD3	PSMD3	PSMD3 26S	PSMD3 26S	Gene_Sym	IPI000116	IPI000116	3	3	3	>IPI:IPI000	1	3	3	3	6.6	6.6	6.6
MAPK1	MAPK1	MAPK1 Mit	MAPK1 Mi	Gene_Sym	IPI000034	IPI000034	2;1	2;1	2;1	>IPI:IPI000	2	2	2	2	5	5	5
FAM49B	FAM49B	FAM49B Pr	FAM49B P	Gene_Sym	IPI003033	IPI003033	4;3;1	4;3;1	4;3;1	>IPI:IPI003	3	4	4	4	14.2	14.2	14.2
C1QBP	C1QBP	C1QBP Cor	C1QBP Cor	Gene_Sym	IPI000142	IPI000142	2;1	2;1	2;1	>IPI:IPI000	2	2	2	2	12.1	12.1	12.1
PPIB	PPIB	PPIB Peptic	PPIB Peptic	Gene_Sym	IPI006463	IPI006463	10;8	10;8	10;8	>IPI:IPI006	2	10	10	10	40.7	40.7	40.7
TRPM2	TRPM2	TRPM2 TRI	TRPM2 TRI	Gene_Sym	IPI008715	IPI008715	1;1;1;1;1	1;1;1;1;1	1;1;1;1;1	>IPI:IPI008	5	1	1	1	0.7	0.7	0.7
CCT2	CCT2	CCT2 T-con	CCT2 T-cor	Gene_Sym	IPI002977	IPI002977	8;1	8;1	8;1	>IPI:IPI002	2	8	8	8	22.1	22.1	22.1
GDI2	GDI2	GDI2 cDNA	GDI2 cDNA	Gene_Sym	IPI000314	IPI000314	11;11;9;7;3	11;11;9;7;3	11;11;9;7;3	>IPI:IPI000	8	11	11	11	33.9	33.9	33.9
EIF3I	EIF3I	EIF3I Eukar	EIF3I Eukar	Gene_Sym	IPI000127	IPI000127	3;1	3;1	3;1	>IPI:IPI000	2	3	3	3	8.6	8.6	8.6
RPLP2	RPLP2	RPLP2 60S	RPLP2 60S	Gene_Sym	IPI000085	IPI000085	4	4	4	>IPI:IPI000	1	4	4	4	69.6	69.6	69.6
PSMD14	PSMD14	PSMD14 26	PSMD14 26	Gene_Sym	IPI000248	IPI000248	1	1	1	>IPI:IPI000	1	1	1	1	4.2	4.2	4.2
RPL24	RPL24	RPL24 19 k	RPL24 19 k	Gene_Sym	IPI007936	IPI007936	2;2;2;2	2;2;2;2	2;2;2;2	>IPI:IPI007	4	2	2	2	10.1	10.1	10.1
AKR1B1	AKR1B1	AKR1B1 Al	AKR1B1 Al	Gene_Sym	IPI004136	IPI004136	3;1;1;1;1;1	3;1;1;1;1;1	3;1;1;1;1;1	>IPI:IPI004	6	3	3	3	8.5	8.5	8.5
PABPC1	PABPC1	PABPC1 Isc	PABPC1 Isc	Gene_Sym	IPI000085	IPI000085	4;4;4;3;2;2	4;4;4;3;2;2	4;4;4;3;2;2	>IPI:IPI000	13	4	4	4	6.4	6.4	6.4
PSMB2	PSMB2	PSMB2 Pro	PSMB2 Prc	Gene_Sym	IPI000280	IPI000280	3;2	3;2	3;2	>IPI:IPI000	2	3	3	3	16.9	16.9	16.9

ILK-2;CCT4	ILK-2;CCT4	ILK-2;CCT4	ILK-2;CCT4	Gene_Sym	IPI0030292	IPI0030292	8;8;7	8;8;7	8;8;7	>IPI:IPI003	3	8	8	8	20	20	20
QARS	QARS	QARS cDN/	QARS cDN/	Gene_Sym	IPI0002666	IPI0002666	7;7;7;7;5;4	7;7;7;7;5;4	7;7;7;7;5;4	>IPI:IPI000	12	7	7	7	10.2	10.2	10.2
RPS25	RPS25	RPS25 40S	RPS25 40S	Gene_Sym	IPI0001275	IPI0001275	4;4;2	4;4;2	4;4;2	>IPI:IPI000	3	4	4	4	24	24	24
SRI	SRI	SRI Sorcin;	SRI Sorcin;	Gene_Sym	IPI0002717	IPI0002717	2;2;2;1	2;2;2;1	2;2;2;1	>IPI:IPI000	4	2	2	2	11.1	11.1	11.1
CNDP2	CNDP2	CNDP2 Isof	CNDP2 Isof	Gene_Sym	IPI0017772	IPI0017772	5;3;3;3;2;2	5;3;3;3;2;2	5;3;3;3;2;2	>IPI:IPI001	7	5	5	5	14.5	14.5	14.5
PSMD8	PSMD8	PSMD8 prc	PSMD8 prc	Gene_Sym	IPI0001020	IPI0001020	2;2;1	2;2;1	2;2;1	>IPI:IPI000	3	2	2	2	7.1	7.1	7.1
RAP1B	RAP1B	RAP1B Ras	RAP1B Ras	Gene_Sym	IPI0001514	IPI0001514	3;3;3;3;2;2	3;3;3;3;2;2	3;3;3;3;2;2	>IPI:IPI000	9	3	3	3	17.9	17.9	17.9
TUFM	TUFM	TUFM Tu tı	TUFM Tu t	Gene_Sym	IPI0002710	IPI0002710	9	9	9	>IPI:IPI000	1	9	9	9	25.3	25.3	25.3
SPTBN1	SPTBN1	SPTBN1 Isc	SPTBN1 Isc	Gene_Sym	IPI0000561	IPI0000561	26;24;24;2	26;24;24;2	26;24;24;2	>IPI:IPI000	10	26	26	26	14	14	14
PSMD11	PSMD11	PSMD11 Pı	PSMD11 Pı	Gene_Sym	IPI0010559	IPI0010559	6;4	6;4	6;4	>IPI:IPI001	2	6	6	6	17.5	17.5	17.5
CCT7	CCT7	CCT7 T-cor	CCT7 T-cor	Gene_Sym	IPI0001846	IPI0001846	7;7;6;4;1	7;7;6;4;1	7;7;6;4;1	>IPI:IPI000	5	7	7	7	16.9	16.9	16.9
EIF4H	EIF4H	EIF4H Simil	EIF4H Simi	Gene_Sym	IPI0037512	IPI0037512	2;2	2;2	2;2	>IPI:IPI003	2	2	2	2	12.2	12.2	12.2
ERP29	ERP29	ERP29 End	ERP29 End	Gene_Sym	IPI0002491	IPI0002491	4;1;1	4;1;1	4;1;1	>IPI:IPI000	3	4	4	4	18	18	18
RPL23	RPL23	RPL23 60S	RPL23 60S	Gene_Sym	IPI0001015	IPI0001015	3;3;2;2;2;1	3;3;2;2;2;1	3;3;2;2;2;1	>IPI:IPI000	6	3	3	3	27.1	27.1	27.1
PGD	PGD	PGD 6-pho	PGD 6-pho	Gene_Sym	IPI0021952	IPI0021952	8;5;3	8;5;3	8;5;3	>IPI:IPI002	3	8	8	8	20.9	20.9	20.9
CXorf26	CXorf26	CXorf26 UI	CXorf26 UI	Gene_Sym	IPI0010710	IPI0010710	2;1	2;1	2;1	>IPI:IPI001	2	2	2	2	9	9	9
VPS35	VPS35	VPS35 Vacı	VPS35 Vac	Gene_Sym	IPI0001893	IPI0001893	5;1	5;1	5;1	>IPI:IPI000	2	5	5	5	6.5	6.5	6.5
#VALUE!	#VALUE!	#VALUE!	#VALUE!	#VALUE!	IPI0001329	IPI0001329	8;5;5;3	8;5;5;3	8;5;5;3	>IPI:IPI000	4	8	8	8	42.8	42.8	42.8
CRKL	CRKL	CRKL Crk-li	CRKL Crk-li	Gene_Sym	IPI0000483	IPI0000483	2	2	2	>IPI:IPI000	1	2	2	2	9.2	9.2	9.2
RANBP1	RANBP1	RANBP1 Pu	RANBP1 Pu	Gene_Sym	IPI0087861	IPI0087861	4;4;4;4;3;3	4;4;4;4;3;3	4;4;4;4;3;3	>IPI:IPI008	10	4	4	4	13.3	13.3	13.3
PDIA6	PDIA6	PDIA6 Isof	PDIA6 Isof	Gene_Sym	IPI0029957	IPI0029957	5;5	5;5	5;5	>IPI:IPI002	2	5	5	5	16.3	16.3	16.3
VARS	VARS	VARS Valyl	VARS Valyl	Gene_Sym	IPI0000087	IPI0000087	3;3;2;2;2;2	3;3;2;2;2;2	3;3;2;2;2;2	>IPI:IPI000	8	3	3	3	2.7	2.7	2.7
EDF1	EDF1	EDF1 Isofo	EDF1 Isofo	Gene_Sym	IPI0002157	IPI0002157	2;2;2	2;2;2	2;2;2	>IPI:IPI000	3	2	2	2	12.2	12.2	12.2
PSMB3	PSMB3	PSMB3 Pro	PSMB3 Prc	Gene_Sym	IPI0002800	IPI0002800	3;2;2	3;2;2	3;2;2	>IPI:IPI000	3	3	3	3	20	20	20
FDPS	FDPS	FDPS Farne	FDPS Farn	Gene_Sym	IPI0091456	IPI0091456	3;3;1;1	3;3;1;1	3;3;1;1	>IPI:IPI009	4	3	3	3	8.8	8.8	8.8
PNP	PNP	PNP cDNA	PNP cDNA	Gene_Sym	IPI0001767	IPI0001767	3	3	3	>IPI:IPI000	1	3	3	3	12.6	12.6	12.6
SSBP1	SSBP1	SSBP1 Sing	SSBP1 Sing	Gene_Sym	IPI0002974	IPI0002974	4;3;3;3	4;3;3;3	4;3;3;3	>IPI:IPI000	4	4	4	4	33.1	33.1	33.1
EIF2B1	EIF2B1	EIF2B1 Trai	EIF2B1 Tra	Gene_Sym	IPI0022130	IPI0022130	2;2;2;1	2;2;2;1	2;2;2;1	>IPI:IPI002	4	2	2	2	7.5	7.5	7.5
LAP3	LAP3	LAP3 Isofo	LAP3 Isofo	Gene_Sym	IPI0041923	IPI0041923	4;4;2	4;4;2	4;4;2	>IPI:IPI004	3	4	4	4	9.2	9.2	9.2
RAB1A	RAB1A	RAB1A Isof	RAB1A Isof	Gene_Sym	IPI0000571	IPI0000571	4;4;4;4;4;4	4;4;4;4;4;4	3;3;3;3;3;3	>IPI:IPI000	22	4	4	3	21	21	15.6
RAB7A	RAB7A	RAB7A Ras	RAB7A Ras	Gene_Sym	IPI0001634	IPI0001634	6;5;4;4;4;4	6;5;4;4;4;4	6;5;4;4;4;4	>IPI:IPI000	11	6	6	6	33.3	33.3	33.3
CS	CS	C	CS Citrate s	CS Citrate s	Gene_Sym	IPI0002536	IPI0002536	6;5;5;2;2;2	6;5;5;2;2;2	6;5;5;2;2;2	>IPI:IPI000	9	6	6	6	13.3	13.3	13.3
CSE1L	CSE1L	CSE1L Isofo	CSE1L Isofo	Gene_Sym	IPI0002274	IPI0002274	14;14;9;8;3	14;14;9;8;3	14;14;9;8;3	>IPI:IPI000	5	14	14	14	17.8	17.8	17.8
RPS26	RPS26	RPS26 Ribo	RPS26 Ribo	Gene_Sym	IPI0040181	IPI0040181	2;2;2;1;1;1	2;2;2;1;1;1	2;2;2;1;1;1	>IPI:IPI004	11	2	2	2	20.9	20.9	20.9
EIF2S1	EIF2S1	EIF2S1 Euk	EIF2S1 Euk	Gene_Sym	IPI0021967	IPI0021967	3	3	3	>IPI:IPI002	1	3	3	3	11.1	11.1	11.1
PSMA5	PSMA5	PSMA5 Pro	PSMA5 Prc	Gene_Sym	IPI0029192	IPI0029192	3	3	3	>IPI:IPI002	1	3	3	3	12	12	12
EIF4E	EIF4E	EIF4E euka	EIF4E euka	Gene_Sym	IPI0090841	IPI0090841	2;2;2;2;1	2;2;2;2;1	2;2;2;2;1	>IPI:IPI009	5	2	2	2	6	6	6
#VALUE!	#VALUE!	#VALUE!	#VALUE!	#VALUE!	IPI0039648	IPI0039648	12;12;9;9;7	12;12;9;9;7	12;12;9;9;7	>IPI:IPI003	15	12	12	12	28.8	28.8	28.8
NUDT21	NUDT21	NUDT21 Cl	NUDT21 Cl	Gene_Sym	IPI0064691	IPI0064691	5	5	5	>IPI:IPI006	1	5	5	5	27.8	27.8	27.8
TAGLN2	TAGLN2	TAGLN2 24	TAGLN2 24	Gene_Sym	IPI0064791	IPI0064791	8;8;8	8;8;8	8;8;8	>IPI:IPI006	3	8	8	8	46.4	46.4	46.4
PRKDC	PRKDC	PRKDC Isof	PRKDC Isof	Gene_Sym	IPI0029633	IPI0029633	9;9;9	9;9;9	9;9;9	>IPI:IPI002	3	9	9	9	2.3	2.3	2.3

RPL11	RPL11	RPL11 Isof	RPL11 Isof	Gene_Sym	IPI003767	IPI003767	2;2;1;1;1	2;2;1;1;1	2;2;1;1;1	>IPI:IPI003	5	2	2	2	12.9	12.9	12.9
RPLP0	RPLP0	RPLP0 60S	RPLP0 60S	Gene_Sym	IPI000085	IPI000085	7;6;6;5;5;5	7;6;6;5;5;5	7;6;6;5;5;5	>IPI:IPI000	12	7	7	7	34.4	34.4	34.4
GTF2I	GTF2I	GTF2I Isofc	GTF2I Isofc	Gene_Sym	IPI000540	IPI000540	4;4;4;4;4;2	4;4;4;4;4;2	4;4;4;4;4;2	>IPI:IPI000	7	4	4	4	4.8	4.8	4.8
SNRPD3	SNRPD3	SNRPD3 Pu	SNRPD3 Pu	Gene_Sym	IPI008797	IPI008797	2;2;2	2;2;2	2;2;2	>IPI:IPI008	3	2	2	2	10.9	10.9	10.9
OLA1	OLA1	OLA1 47 kI	OLA1 47 kI	Gene_Sym	IPI009168	IPI009168	2;2;2;2;1	2;2;2;2;1	2;2;2;2;1	>IPI:IPI009	5	2	2	2	6.2	6.2	6.2
ACTR2	ACTR2	ACTR2 acti	ACTR2 acti	Gene_Sym	IPI004705	IPI004705	2;2;2	2;2;2	2;2;2	>IPI:IPI004	3	2	2	2	6.8	6.8	6.8
PSMC2	PSMC2	PSMC2 26S	PSMC2 26S	Gene_Sym	IPI000214	IPI000214	3;1;1	3;1;1	3;1;1	>IPI:IPI000	3	3	3	3	7.6	7.6	7.6
SERPINB1	SERPINB1	SERPINB1 I	SERPINB1 I	Gene_Sym	IPI000274	IPI000274	2	2	2	>IPI:IPI000	1	2	2	2	6.6	6.6	6.6
UBE2M	UBE2M	UBE2M NE	UBE2M NE	Gene_Sym	IPI000225	IPI000225	2	2	2	>IPI:IPI000	1	2	2	2	10.9	10.9	10.9
PSMA7	PSMA7	PSMA7 Iso	PSMA7 Iso	Gene_Sym	IPI000241	IPI000241	6;5;4;4;4;4	6;5;4;4;4;4	6;5;4;4;4;4	>IPI:IPI000	8	6	6	6	34.3	34.3	34.3
LDHA	LDHA	LDHA lacta	LDHA lacta	Gene_Sym	IPI009471	IPI009471	12;12;11;1	12;12;11;1	11;11;10;1	>IPI:IPI009	8	12	12	11	36.8	36.8	33.5
EIF3A	EIF3A	EIF3A Euka	EIF3A Euka	Gene_Sym	IPI000290	IPI000290	10	10	10	>IPI:IPI000	1	10	10	10	7.7	7.7	7.7
IDH2	IDH2	IDH2 Isocit	IDH2 Isocit	Gene_Sym	IPI000111	IPI000111	11;8;1;1;1;	11;8;1;1;1;	11;8;1;1;1;	>IPI:IPI000	6	11	11	11	26.5	26.5	26.5
RPS14	RPS14	RPS14 40S	RPS14 40S	Gene_Sym	IPI000262	IPI000262	2	2	2	>IPI:IPI000	1	2	2	2	15.9	15.9	15.9
TALDO1	TALDO1	TALDO1 Tr	TALDO1 Tr	Gene_Sym	IPI007446	IPI007446	8	8	8	>IPI:IPI007	1	8	8	8	25.5	25.5	25.5
SHMT2	SHMT2	SHMT2 Ser	SHMT2 Ser	Gene_Sym	IPI000025	IPI000025	12;12;12;1	12;12;12;1	12;12;12;1	>IPI:IPI000	18	12	12	12	25.2	25.2	25.2
RPIA	RPIA	RPIA Ribos	RPIA Ribos	Gene_Sym	IPI000265	IPI000265	2	2	2	>IPI:IPI000	1	2	2	2	5.1	5.1	5.1
LDHB	LDHB	LDHB L-lact	LDHB L-lac	Gene_Sym	IPI002192	IPI002192	11;6;5;1;1	10;5;5;0;0	10;5;5;0;0	>IPI:IPI002	5	11	10	10	34.4	30.8	30.8
BSG	BSG	BSG Isofor	BSG Isofor	Gene_Sym	IPI002180	IPI002180	2;2;2;1	2;2;2;1	2;2;2;1	>IPI:IPI002	4	2	2	2	6.2	6.2	6.2
ANXA7	ANXA7	ANXA7 Isof	ANXA7 Iso	Gene_Sym	IPI000024	IPI000024	4;4;4	4;4;4	4;4;4	>IPI:IPI000	3	4	4	4	9.4	9.4	9.4
#VALUE!	#VALUE!	#VALUE!	#VALUE!	#VALUE!	IPI000159	IPI000159	2;1;1;1	2;1;1;1	2;1;1;1	>IPI:IPI000	4	2	2	2	11.6	11.6	11.6
RPL19	RPL19	RPL19 60S	RPL19 60S	Gene_Sym	IPI000253	IPI000253	2;1	2;1	2;1	>IPI:IPI000	2	2	2	2	13.3	13.3	13.3
RPL28	RPL28	RPL28 ribo	RPL28 ribo	Gene_Sym	IPI009145	IPI009145	3;3;3;3;3	3;3;3;3;3	3;3;3;3;3	>IPI:IPI009	5	3	3	3	17.2	17.2	17.2
MARS	MARS	MARS Met	MARS Met	Gene_Sym	IPI000082	IPI000082	6;5;1;1;1;1	6;5;1;1;1;1	6;5;1;1;1;1	>IPI:IPI000	6	6	6	6	8.7	8.7	8.7
PDCD4	PDCD4	PDCD4 Pro	PDCD4 Pro	Gene_Sym	IPI002901	IPI002901	3;3;3;1	3;3;3;1	3;3;3;1	>IPI:IPI002	4	3	3	3	10	10	10
HSPH1	HSPH1	HSPH1 Isof	HSPH1 Isof	Gene_Sym	IPI009391	IPI009391	15;15;14;1	15;15;14;1	13;13;12;1	>IPI:IPI009	10	15	15	13	20.2	20.2	17.6
GNAS	GNAS	GNAS Isofc	GNAS Isofc	Gene_Sym	IPI000958	IPI000958	1;1;1;1;1;1	1;1;1;1;1;1	1;1;1;1;1;1	>IPI:IPI000	22	1	1	1	1.1	1.1	1.1
GOT2	GOT2	GOT2 Aspa	GOT2 Aspa	Gene_Sym	IPI000182	IPI000182	9;7;1	9;7;1	9;7;1	>IPI:IPI000	3	9	9	9	23	23	23
RPL10A	RPL10A	RPL10A 60	RPL10A 60	Gene_Sym	IPI004125	IPI004125	2;1;1	2;1;1	2;1;1	>IPI:IPI004	3	2	2	2	9.7	9.7	9.7
EEF2	EEF2	EEF2 Elong	EEF2 Elong	Gene_Sym	IPI001862	IPI001862	31;22;7;1;1	31;22;7;1;1	31;22;7;1;1	>IPI:IPI001	5	31	31	31	44.9	44.9	44.9
RPL26	RPL26	RPL26 Puta	RPL26 Puta	Gene_Sym	IPI004338	IPI004338	3;3;3;3;2;1	3;3;3;3;2;1	3;3;3;3;2;1	>IPI:IPI004	6	3	3	3	15.7	15.7	15.7
PSMC5	PSMC5	PSMC5 26S	PSMC5 26S	Gene_Sym	IPI000239	IPI000239	2;2;2;1	2;2;2;1	2;2;2;1	>IPI:IPI000	4	2	2	2	6.7	6.7	6.7
EIF3E	EIF3E	EIF3E Euka	EIF3E Euka	Gene_Sym	IPI000130	IPI000130	9;5	9;5	9;5	>IPI:IPI000	2	9	9	9	18	18	18
DDX5	DDX5	DDX5 Prob	DDX5 Prob	Gene_Sym	IPI000176	IPI000176	3;3;1;1;1;1	3;3;1;1;1;1	3;3;1;1;1;1	>IPI:IPI000	9	3	3	3	4.9	4.9	4.9
LRPPRC	LRPPRC	LRPPRC Le	LRPPRC Le	Gene_Sym	IPI007832	IPI007832	24;6;6;5	24;6;6;5	24;6;6;5	>IPI:IPI007	4	24	24	24	19.9	19.9	19.9
CCT8	CCT8	CCT8 T-cor	CCT8 T-cor	Gene_Sym	IPI007840	IPI007840	18;18;9;4	18;18;9;4	18;18;9;4	>IPI:IPI007	4	18	18	18	35.8	35.8	35.8
ADSL	ADSL	ADSL Isofo	ADSL Isofo	Gene_Sym	IPI009420	IPI009420	3;2;2;2;1	3;2;2;2;1	3;2;2;2;1	>IPI:IPI009	5	3	3	3	6	6	6
RPL27A	RPL27A	RPL27A 60	RPL27A 60	Gene_Sym	IPI004567	IPI004567	1	1	1	>IPI:IPI004	1	1	1	1	7.4	7.4	7.4
PGK1	PGK1	PGK1 Phos	PGK1 Phos	Gene_Sym	IPI001693	IPI001693	14;10;6;3;3	14;10;6;3;3	14;10;6;3;3	>IPI:IPI001	5	14	14	14	45.1	45.1	45.1
RPS7	RPS7	RPS7 40S ri	RPS7 40S r	Gene_Sym	IPI000134	IPI000134	5;5;4;4;3;2	5;5;4;4;3;2	5;5;4;4;3;2	>IPI:IPI000	6	5	5	5	22.2	22.2	22.2
EIF3J	EIF3J	EIF3J Eukar	EIF3J Eukar	Gene_Sym	IPI002904	IPI002904	2;2	2;2	2;2	>IPI:IPI002	2	2	2	2	7.8	7.8	7.8

RPL12	RPL12	RPL12 Isof	RPL12 Isof	Gene_Sym	IPI000249	IPI000249	5;4;1	5;4;1	5;4;1	>IPI:IPI000	3	5	5	5	49.1	49.1	49.1
HSD17B12	HSD17B12	HSD17B12	HSD17B12	Gene_Sym	IPI000076	IPI000076	2;1	2;1	2;1	>IPI:IPI000	2	2	2	2	8	8	8
GLO1	GLO1	GLO1 Lactc	GLO1 Lactc	Gene_Sym	IPI002207	IPI002207	6	6	6	>IPI:IPI002	1	6	6	6	38.6	38.6	38.6
CACYBP	CACYBP	CACYBP Isc	CACYBP Isc	Gene_Sym	IPI003956	IPI003956	5;5;5;2	5;5;5;2	5;5;5;2	>IPI:IPI003	4	5	5	5	23.7	23.7	23.7
P4HB	P4HB	P4HB Prote	P4HB Prote	Gene_Sym	IPI000107	IPI000107	4;3;1	4;3;1	4;3;1	>IPI:IPI000	3	4	4	4	8.3	8.3	8.3
MAT2B	MAT2B	MAT2B Iso	MAT2B Iso	Gene_Sym	IPI000023	IPI000023	3;3;3;2;2;1	3;3;3;2;2;1	3;3;3;2;2;1	>IPI:IPI000	7	3	3	3	10.2	10.2	10.2
ST13	ST13	ST13 Hsc7(	ST13 Hsc7(	Gene_Sym	IPI000328	IPI000328	5;5;5;4;4;4	5;5;5;4;4;4	5;5;5;4;4;4	>IPI:IPI000	9	5	5	5	15.2	15.2	15.2
NPM1	NPM1	NPM1 Isof	NPM1 Isof	Gene_Sym	IPI005492	IPI005492	3;3;3;1	3;3;3;1	3;3;3;1	>IPI:IPI005	4	3	3	3	14.6	14.6	14.6
MAPRE1	MAPRE1	MAPRE1 M	MAPRE1 M	Gene_Sym	IPI000175	IPI000175	5;5	5;5	5;5	>IPI:IPI000	2	5	5	5	28	28	28
PRDX1	PRDX1	PRDX1 Per	PRDX1 Per	Gene_Sym	IPI000008	IPI000008	9;9;6	8;8;5	6;6;3	>IPI:IPI000	3	9	8	6	39.7	34.2	28.1
PA2G4	PA2G4	PA2G4 PA2	PA2G4 PA2	Gene_Sym	IPI008075	IPI008075	7;7;7;3;1;1	7;7;7;3;1;1	7;7;7;3;1;1	>IPI:IPI008	8	7	7	7	17.2	17.2	17.2
#VALUE!	#VALUE!	#VALUE!	#VALUE!	#VALUE!	IPI000108	IPI000108	6;1	6;1	6;1	>IPI:IPI000	2	6	6	6	28.2	28.2	28.2
HSPA8	HSPA8	HSPA8 Isof	HSPA8 Isof	Gene_Sym	IPI000038	IPI000038	25;21;21;1	25;21;21;1	21;18;18;1	>IPI:IPI000	9	25	25	21	41	41	36.2
RPS16	RPS16	RPS16 40S	RPS16 40S	Gene_Sym	IPI002210	IPI002210	6;6;3	6;6;3	6;6;3	>IPI:IPI002	3	6	6	6	37.7	37.7	37.7
IQGAP1	IQGAP1	IQGAP1 Ra	IQGAP1 Ra	Gene_Sym	IPI000093	IPI000093	18;1	18;1	18;1	>IPI:IPI000	2	18	18	18	13.9	13.9	13.9
PRDX5	PRDX5	PRDX5 Isof	PRDX5 Isof	Gene_Sym	IPI000249	IPI000249	4;4;4;1	4;4;4;1	4;4;4;1	>IPI:IPI000	4	4	4	4	24.8	24.8	24.8
STX7	STX7	STX7 Isofo	STX7 Isofo	Gene_Sym	IPI002898	IPI002898	4;4;3	4;4;3	4;4;3	>IPI:IPI002	3	4	4	4	19.5	19.5	19.5
RPL14	RPL14	RPL14 Ribc	RPL14 Ribc	Gene_Sym	IPI005557	IPI005557	2;2;2;2	2;2;2;2	2;2;2;2	>IPI:IPI005	4	2	2	2	10.9	10.9	10.9
RPS20	RPS20	RPS20 ribo	RPS20 ribo	Gene_Sym	IPI007946	IPI007946	3;3;2;1;1;1	3;3;2;1;1;1	3;3;2;1;1;1	>IPI:IPI007	8	3	3	3	21.1	21.1	21.1
SPTAN1	SPTAN1	SPTAN1 Isc	SPTAN1 Isc	Gene_Sym	IPI008442	IPI008442	49;49;48;4	49;49;48;4	49;49;48;4	>IPI:IPI008	5	49	49	49	23.9	23.9	23.9
RPN1	RPN1	RPN1 Dolic	RPN1 Dolic	Gene_Sym	IPI000258	IPI000258	5;4;1	5;4;1	5;4;1	>IPI:IPI000	3	5	5	5	8.7	8.7	8.7
PPP2CA	PPP2CA	PPP2CA Se	PPP2CA Se	Gene_Sym	IPI000083	IPI000083	2;2;2	2;2;2	2;2;2	>IPI:IPI000	3	2	2	2	8.4	8.4	8.4
RNASEH2C	RNASEH2C	RNASEH2C	RNASEH2C	Gene_Sym	IPI003829	IPI003829	2;2;2	2;2;2	2;2;2	>IPI:IPI003	3	2	2	2	15.2	15.2	15.2
SEC22B	SEC22B	SEC22B Ve	SEC22B Ve	Gene_Sym	IPI000068	IPI000068	3	3	3	>IPI:IPI000	1	3	3	3	16.7	16.7	16.7
EEF1G;TUT	EEF1G;TUT	EEF1G;TUT	EEF1G;TUT	Gene_Sym	IPI000008	IPI000008	13;13;8;7;2	13;13;8;7;2	13;13;8;7;2	>IPI:IPI000	6	13	13	13	28.7	28.7	28.7
PCMT1	PCMT1	PCMT1 Isof	PCMT1 Iso	Gene_Sym	IPI004116	IPI004116	7;6;6;6;2	7;6;6;6;2	7;6;6;6;2	>IPI:IPI004	5	7	7	7	36.1	36.1	36.1
CCT3	CCT3	CCT3 T-cor	CCT3 T-cor	Gene_Sym	IPI005531	IPI005531	11;11;10;4	11;11;10;4	11;11;10;4	>IPI:IPI005	7	11	11	11	22.2	22.2	22.2
RCTPI1;TPI	RCTPI1;TPI	RCTPI1;TPI	RCTPI1;TPI	Gene_Sym	IPI004650	IPI004650	14;14;12;1	14;14;12;1	14;14;12;1	>IPI:IPI004	5	14	14	14	61.2	61.2	61.2
#VALUE!	#VALUE!			Gene_Sym	IPI004146	IPI004146	34;18;9;8;8	34;18;9;8;8	17;6;0;0;6;	>IPI:IPI004	9	34	34	17	42.3	42.3	23.3
PSMD2	PSMD2	PSMD2 26	PSMD2 26	Gene_Sym	IPI000122	IPI000122	2;2;2;2;2;2	2;2;2;2;2;2	2;2;2;2;2;2	>IPI:IPI000	6	2	2	2	2.6	2.6	2.6
PFN1	PFN1	PFN1 Profi	PFN1 Profi	Gene_Sym	IPI002166	IPI002166	4;1	4;1	4;1	>IPI:IPI002	2	4	4	4	41.4	41.4	41.4
#VALUE!	#VALUE!	EIF4A1;SN(	EIF4A1;SN(	Gene_Sym	IPI000254	IPI000254	8;3	8;3	3;1	>IPI:IPI000	2	8	8	3	21.7	21.7	7.9
SDHB	SDHB	SDHB Succ	SDHB Succ	Gene_Sym	IPI002949	IPI002949	3	3	3	>IPI:IPI002	1	3	3	3	10.7	10.7	10.7
#VALUE!	#VALUE!	#VALUE!	#VALUE!	#VALUE!	IPI000212	IPI000212	10;6;2;2	8;5;1;1	7;4;1;1	>IPI:IPI000	4	10	8	7	46.9	39.6	35.9
ACAA2	ACAA2	ACAA2 3-k	ACAA2 3-k	Gene_Sym	IPI000015	IPI000015	3;3	3;3	3;3	>IPI:IPI000	2	3	3	3	8.3	8.3	8.3
YWHAE	YWHAE	YWHAE 14	YWHAE 14	Gene_Sym	IPI000008	IPI000008	11;8;5;4;3;	11;8;5;4;3;	9;7;5;3;2;2	>IPI:IPI000	7	11	11	9	43.9	43.9	36.9
GPI	GPI	GPI Glucos	GPI Glucos	Gene_Sym	IPI009107	IPI009107	7;7;7;2;1	7;7;7;2;1	7;7;7;2;1	>IPI:IPI009	5	7	7	7	14.4	14.4	14.4
MCM7	MCM7	MCM7 Isof	MCM7 Isof	Gene_Sym	IPI002999	IPI002999	8;8;3;2	8;8;3;2	8;8;3;2	>IPI:IPI002	4	8	8	8	15.2	15.2	15.2
RPS12	RPS12	RPS12 40S	RPS12 40S	Gene_Sym	IPI000139	IPI000139	3;1	3;1	3;1	>IPI:IPI000	2	3	3	3	20.5	20.5	20.5
SYNGR2	SYNGR2	SYNGR2 SY	SYNGR2 SY	Gene_Sym	IPI006547	IPI006547	2;2;2;1;1	2;2;2;1;1	2;2;2;1;1	>IPI:IPI006	5	2	2	2	7.3	7.3	7.3
EIF4G1	EIF4G1	EIF4G1 EIF	EIF4G1 EIF	Gene_Sym	IPI009254	IPI009254	4;4;4;4;4;4	4;4;4;4;4;4	4;4;4;4;4;4	>IPI:IPI009	21	4	4	4	3.5	3.5	3.5

LTA4H	LTA4H	LTA4H Isof	LTA4H Isof	Gene_Sym	IPI0021907	IPI0021907	2;1;1;1;1;1	2;1;1;1;1;1	2;1;1;1;1;1	>IPI:IPI002	6	2	2	2	5.1	5.1	5.1
HSP90AB2	HSP90AB2I	HSP90AB2I	HSP90AB2	Gene_Sym	IPI0045559	IPI0045559	7	1	1	>IPI:IPI004	1	7	1	1	14.7	3.6	3.6
GARS	GARS	GARS Glyc	GARS Glyc	Gene_Sym	IPI0078309	IPI0078309	6;6	6;6	6;6	>IPI:IPI007	2	6	6	6	9.7	9.7	9.7
MYL12A	MYL12A	MYL12A M	MYL12A M	Gene_Sym	IPI0060452	IPI0060452	3;3;3;3;2;1	3;3;3;3;2;1	3;3;3;3;2;1	>IPI:IPI006	9	3	3	3	18.1	18.1	18.1
RPL22	RPL22	RPL22 60S	RPL22 60S	Gene_Sym	IPI0021915	IPI0021915	2;2;1	2;2;1	2;2;1	>IPI:IPI002	3	2	2	2	18.8	18.8	18.8
PSMA1	PSMA1	PSMA1 Iso	PSMA1 Iso	Gene_Sym	IPI0047244	IPI0047244	5;5;5;2;2	5;5;5;2;2	5;5;5;2;2	>IPI:IPI004	5	5	5	5	20.4	20.4	20.4
C14orf166	C14orf166	C14orf166	C14orf166	Gene_Sym	IPI0000698	IPI0000698	6;6	6;6	6;6	>IPI:IPI000	2	6	6	6	32	32	32
PDIA4	PDIA4	PDIA4 Prot	PDIA4 Prot	Gene_Sym	IPI0000990	IPI0000990	3;2	3;2	3;2	>IPI:IPI000	2	3	3	3	5.1	5.1	5.1
YWHAB	YWHAB	YWHAB Iso	YWHAB Isc	Gene_Sym	IPI0021631	IPI0021631	9;9;3;3;2;2	6;6;2;2;0;0	5;5;1;1;0;0	>IPI:IPI002	8	9	6	5	40.7	29.7	23.2
#VALUE!	#VALUE!	#VALUE!	#VALUE!	#VALUE!	IPI0030459	IPI0030459	5;4;4;4;3;2	4;3;4;3;2;1	4;3;4;3;2;1	>IPI:IPI003	7	5	4	4	11.7	10	10
RPL23A	RPL23A	RPL23A Rib	RPL23A Rib	Gene_Sym	IPI0078915	IPI0078915	2;2;2;2;2;1	2;2;2;2;2;1	2;2;2;2;2;1	>IPI:IPI007	8	2	2	2	10.8	10.8	10.8
HMGB1	HMGB1	HMGB1	HMGB1	Gene_Sym	IPI0041925	IPI0041925	10;9;9;9;9;	10;9;9;9;9;	8;8;8;8;8;6	>IPI:IPI004	16	10	10	8	40.5	40.5	30.7
RPS19	RPS19	RPS19 40S	RPS19 40S	Gene_Sym	IPI0021578	IPI0021578	7	7	7	>IPI:IPI002	1	7	7	7	40	40	40
#VALUE!	#VALUE!	#VALUE!	#VALUE!	#VALUE!	IPI0064545	IPI0064545	20;19;18;1	20;19;18;1	4;4;3;0;4;3	>IPI:IPI006	17	20	20	4	58	58	10.6
#VALUE!	#VALUE!	#VALUE!	#VALUE!	#VALUE!	IPI0084397	IPI0084397	8;8;2;1	8;8;2;1	4;4;0;0	>IPI:IPI008	4	8	8	4	13.3	13.3	7.5
EEF1D	EEF1D	EEF1D Isof	EEF1D Isof	Gene_Sym	IPI0064297	IPI0064297	8;8;8;6;5;4	8;8;8;6;5;4	8;8;8;6;5;4	>IPI:IPI006	7	8	8	8	16.4	16.4	16.4
NACA	NACA	NACA nasc	NACA nasc	Gene_Sym	IPI0079712	IPI0079712	3;3;3;3	3;3;3;3	3;3;3;3	>IPI:IPI007	4	3	3	3	4.5	4.5	4.5
TNPO1	TNPO1	TNPO1 Isof	TNPO1 Iso	Gene_Sym	IPI0002436	IPI0002436	2;2;2;1;1;1	2;2;2;1;1;1	2;2;2;1;1;1	>IPI:IPI000	6	2	2	2	2.4	2.4	2.4
AHCY	AHCY	AHCY Aden	AHCY Ader	Gene_Sym	IPI0001200	IPI0001200	11;10	11;10	11;10	>IPI:IPI000	2	11	11	11	28.7	28.7	28.7
PTGES3	PTGES3	PTGES3 Pro	PTGES3 Pro	Gene_Sym	IPI0078910	IPI0078910	3;3;3;3;3;2	3;3;3;3;3;2	3;3;3;3;3;2	>IPI:IPI007	7	3	3	3	18.2	18.2	18.2
ESD	ESD	ESD S-form	ESD S-form	Gene_Sym	IPI0041170	IPI0041170	4;4;3	4;4;3	4;4;3	>IPI:IPI004	3	4	4	4	15.6	15.6	15.6
VCL	VCL	VCL Isoforr	VCL Isoforr	Gene_Sym	IPI0030716	IPI0030716	3;3;1;1	3;3;1;1	3;3;1;1	>IPI:IPI003	4	3	3	3	2.7	2.7	2.7
TLN1	TLN1	TLN1 Talin	TLN1 Talin	Gene_Sym	IPI0029895	IPI0029895	20;4	20;4	20;4	>IPI:IPI002	2	20	20	20	10.4	10.4	10.4
NSF	NSF	NSF Vesicle	NSF Vesicle	Gene_Sym	IPI0000645	IPI0000645	5;5;3;1	5;5;3;1	5;5;3;1	>IPI:IPI000	4	5	5	5	7.5	7.5	7.5
RFC4	RFC4	RFC4 Repli	RFC4 Repli	Gene_Sym	IPI0001738	IPI0001738	3;2;2;1;1;1	3;2;2;1;1;1	3;2;2;1;1;1	>IPI:IPI000	7	3	3	3	9.4	9.4	9.4
HMGB2	HMGB2	HMGB2 Hig	HMGB2 Hig	Gene_Sym	IPI0021905	IPI0021905	4	2	2	>IPI:IPI002	1	4	2	2	17.2	7.2	7.2
HADHB	HADHB	HADHB Trif	HADHB Tri	Gene_Sym	IPI0002275	IPI0002275	3;2;2;2;2;1	3;2;2;2;2;1	3;2;2;2;2;1	>IPI:IPI000	6	3	3	3	6.1	6.1	6.1
FUBP1	FUBP1	FUBP1 cDN	FUBP1 cDN	Gene_Sym	IPI0064194	IPI0064194	4;4;4;4;4	2;2;2;2;2	2;2;2;2;2	>IPI:IPI006	5	4	2	2	4.4	3.2	3.2
UBE2N	UBE2N	UBE2N Ubi	UBE2N Ubi	Gene_Sym	IPI0000394	IPI0000394	4;4;3;3;2	4;4;3;3;2	4;4;3;3;2	>IPI:IPI000	5	4	4	4	23.7	23.7	23.7
ENO1	ENO1	ENO1 Isofo	ENO1 Isofo	Gene_Sym	IPI0046524	IPI0046524	22;15	22;15	21;15	>IPI:IPI004	2	22	22	21	52.1	52.1	47.9
RUVBL2	RUVBL2	RUVBL2 Ru	RUVBL2 Ru	Gene_Sym	IPI0000910	IPI0000910	4;2	4;2	4;2	>IPI:IPI000	2	4	4	4	10.2	10.2	10.2
IMMT	IMMT	IMMT Isofo	IMMT Isofo	Gene_Sym	IPI0000996	IPI0000996	4;4;4;4;4;4	4;4;4;4;4;4	4;4;4;4;4;4	>IPI:IPI000	11	4	4	4	6.5	6.5	6.5
EEF1B2	EEF1B2	EEF1B2 Elo	EEF1B2 Elo	Gene_Sym	IPI0017847	IPI0017847	2;1;1;1	2;1;1;1	2;1;1;1	>IPI:IPI001	4	2	2	2	12.4	12.4	12.4
RUVBL1	RUVBL1	RUVBL1 Isc	RUVBL1 Isc	Gene_Sym	IPI0002118	IPI0002118	7;6;3;3;2;1	7;6;3;3;2;1	7;6;3;3;2;1	>IPI:IPI000	6	7	7	7	21.1	21.1	21.1
PSMA3	PSMA3	PSMA3 Iso	PSMA3 Iso	Gene_Sym	IPI0041924	IPI0041924	3;3	3;3	3;3	>IPI:IPI004	2	3	3	3	12.2	12.2	12.2
CDC2	CDC2	CDC2 Putat	CDC2 Puta	Gene_Sym	IPI0002668	IPI0002668	6;6;5;2;2;2	6;6;5;2;2;2	5;5;5;1;1;1	>IPI:IPI000	41	6	6	5	24.8	24.8	22.1
#VALUE!	#VALUE!	#VALUE!	#VALUE!	#VALUE!	IPI0000827	IPI0000827	2;2;1;1;1;1	2;2;1;1;1;1	2;2;1;1;1;1	>IPI:IPI000	11	2	2	2	6.5	6.5	6.5
#VALUE!	#VALUE!	#VALUE!	#VALUE!	#VALUE!	IPI0029915	IPI0029915	5;5;4;4;3;2	5;5;4;4;3;2	5;5;4;4;3;2	>IPI:IPI002	6	5	5	5	16.1	16.1	16.1
CFL1	CFL1	CFL1 Cofili	CFL1 Cofili	Gene_Sym	IPI0001201	IPI0001201	5;4;1	5;4;1	5;4;1	>IPI:IPI000	3	5	5	5	38.6	38.6	38.6
VCP	VCP	VCP Transi	VCP Transi	Gene_Sym	IPI0002277	IPI0002277	20;4;4	20;4;4	20;4;4	>IPI:IPI000	3	20	20	20	28.3	28.3	28.3
-	-	24 - 24 kDa pr	- 24 kDa pr	Gene_Sym	IPI0039761	IPI0039761	3;3;1	3;3;1	3;3;1	>IPI:IPI003	3	3	3	3	14.2	14.2	14.2

RPS8	RPS8	RPS8 40S ri	RPS8 40S r	Gene_Sym	IPI002165	IPI002165	3;3	3;3	3;3	>IPI:IPI002	2	3	3	3	18.8	18.8	18.8
TARS	TARS	TARS cDNA	TARS cDNA	Gene_Sym	IPI009089	IPI009089	3;3;3	3;3;3	3;3;3	>IPI:IPI009	3	3	3	3	4.8	4.8	4.8
APEX1	APEX1	APEX1 DNA	APEX1 DN	Gene_Sym	IPI002159	IPI002159	5;1	5;1	5;1	>IPI:IPI002	2	5	5	5	21.7	21.7	21.7
RPL18	RPL18	RPL18 60S	RPL18 60S	Gene_Sym	IPI002157	IPI002157	2;1	2;1	2;1	>IPI:IPI002	2	2	2	2	13.8	13.8	13.8
CCT5	CCT5	CCT5 T-con	CCT5 T-cor	Gene_Sym	IPI000107	IPI000107	7;7;6	7;7;6	7;7;6	>IPI:IPI000	3	7	7	7	14.8	14.8	14.8
#VALUE!	#VALUE!	RPSAP15;R	RPSAP15;R	Gene_Sym	IPI004131	IPI004131	6;6;6;5;5;5	6;6;6;5;5;5	6;6;6;5;5;5	>IPI:IPI004	16	6	6	6	24.7	24.7	24.7
PTBP1	PTBP1	PTBP1 poly	PTBP1 poly	Gene_Sym	IPI001836	IPI001836	3;3;3;2;1;1	3;3;3;2;1;1	3;3;3;2;1;1	>IPI:IPI001	10	3	3	3	9.2	9.2	9.2
SKP1	SKP1	SKP1 Isofo	SKP1 Isofo	Gene_Sym	IPI003013	IPI003013	2;1;1	2;1;1	2;1;1	>IPI:IPI003	3	2	2	2	15.3	15.3	15.3
GCN1L1	GCN1L1	GCN1L1 Tr	GCN1L1 Tr	Gene_Sym	IPI000011	IPI000011	25;1;1	25;1;1	25;1;1	>IPI:IPI000	3	25	25	25	12.4	12.4	12.4
-	-	27 - 27 kDa pr	- 27 kDa pr	Gene_Sym	IPI007928	IPI007928	1;1;1;1;1;1	1;1;1;1;1;1	1;1;1;1;1;1	>IPI:IPI007	6	1	1	1	6.1	6.1	6.1
PARP1	PARP1	PARP1 Poly	PARP1 Poly	Gene_Sym	IPI004490	IPI004490	3;1	3;1	3;1	>IPI:IPI004	2	3	3	3	3.6	3.6	3.6
PRDX6	PRDX6	PRDX6 Per	PRDX6 Per	Gene_Sym	IPI002203	IPI002203	8;2	8;2	8;2	>IPI:IPI002	2	8	8	8	39.3	39.3	39.3
ARHGDIB	ARHGDIB	ARHGDIB R	ARHGDIB R	Gene_Sym	IPI000038	IPI000038	5;5;4;3;1	5;5;4;3;1	5;5;4;3;1	>IPI:IPI000	5	5	5	5	35.8	35.8	35.8
DUT	DUT	DUT Isofor	DUT Isofor	Gene_Sym	IPI000136	IPI000136	1;1;1;1;1	1;1;1;1;1	1;1;1;1;1	>IPI:IPI000	5	1	1	1	4	4	4
GAPDH	GAPDH	GAPDH	GAPDH	Gene_Sym	IPI002190	IPI002190	8;8;8;6;6;4	8;8;8;6;6;4	8;8;8;6;6;4	>IPI:IPI002	9	8	8	8	34.9	34.9	34.9
UBA1	UBA1	UBA1 Ubiq	UBA1 Ubiq	Gene_Sym	IPI006450	IPI006450	17;8;6;4;4;	17;8;6;4;4;	17;8;6;4;4;	>IPI:IPI006	9	17	17	17	22.8	22.8	22.8
GLOD4	GLOD4	GLOD4 Un	GLOD4 Un	Gene_Sym	IPI000071	IPI000071	2;2;2;2;2;1	2;2;2;2;2;1	2;2;2;2;2;1	>IPI:IPI000	6	2	2	2	4	4	4
PCNA	PCNA	PCNA Proli	PCNA Proli	Gene_Sym	IPI000217	IPI000217	7	7	7	>IPI:IPI000	1	7	7	7	31	31	31
-	-	Pu - Putative u	- Putative u	Gene_Sym	IPI008723	IPI008723	2;2;2;2;2;2	2;2;2;2;2;2	2;2;2;2;2;2	>IPI:IPI008	7	2	2	2	9.2	9.2	9.2
EIF5A	EIF5A	EIF5A Isofo	EIF5A Isofo	Gene_Sym	IPI003760	IPI003760	3;3;3;1;1;1	3;3;3;1;1;1	3;3;3;1;1;1	>IPI:IPI003	7	3	3	3	10.3	10.3	10.3
SNRPD2	SNRPD2	SNRPD2 Sn	SNRPD2 Sr	Gene_Sym	IPI000179	IPI000179	6;5;4;2	6;5;4;2	6;5;4;2	>IPI:IPI000	4	6	6	6	46.6	46.6	46.6
EIF3K	EIF3K	EIF3K Euka	EIF3K Euka	Gene_Sym	IPI000331	IPI000331	2	2	2	>IPI:IPI000	1	2	2	2	11.5	11.5	11.5
ANP32E	ANP32E	ANP32E Ac	ANP32E Ac	Gene_Sym	IPI001653	IPI001653	2;2	2;2	2;2	>IPI:IPI001	2	2	2	2	5.2	5.2	5.2
SFPQ	SFPQ	SFPQ Isofo	SFPQ Isofo	Gene_Sym	IPI000107	IPI000107	7;6	7;6	6;5	>IPI:IPI000	2	7	7	6	13	13	11.9
CAT	CAT	CAT Catala	CAT Catala	Gene_Sym	IPI004654	IPI004654	3	3	3	>IPI:IPI004	1	3	3	3	8.7	8.7	8.7
NAP1L1	NAP1L1	NAP1L1 Nu	NAP1L1 Nu	Gene_Sym	IPI000238	IPI000238	5;5;5;5;3	5;5;5;5;3	4;4;4;4;2	>IPI:IPI000	5	5	5	4	17.1	17.1	14.6
PSMC3	PSMC3	PSMC3 26S	PSMC3 26S	Gene_Sym	IPI000183	IPI000183	6	6	6	>IPI:IPI000	1	6	6	6	16.6	16.6	16.6
DCTN3	DCTN3	DCTN3 Isof	DCTN3 Isof	Gene_Sym	IPI000270	IPI000270	2;2;2;2;2	2;2;2;2;2	2;2;2;2;2	>IPI:IPI000	5	2	2	2	10.2	10.2	10.2
STMN2	STMN2	STMN2 Sta	STMN2 Sta	Gene_Sym	IPI002186	IPI002186	3;3;2;1;1;1	1;1;0;0;0;0	1;1;0;0;0;0	>IPI:IPI002	7	3	1	1	15.1	5.6	5.6
DCTN2	DCTN2	DCTN2 dyn	DCTN2 dyr	Gene_Sym	IPI002205	IPI002205	3;3;1	3;3;1	3;3;1	>IPI:IPI002	3	3	3	3	10.8	10.8	10.8
NSFL1C	NSFL1C	NSFL1C Iso	NSFL1C Iso	Gene_Sym	IPI003975	IPI003975	3;3;3;2;1	3;3;3;2;1	3;3;3;2;1	>IPI:IPI003	5	3	3	3	9.1	9.1	9.1
RNASEH2A	RNASEH2A	RNASEH2A	RNASEH2A	Gene_Sym	IPI002901	IPI002901	3	3	3	>IPI:IPI002	1	3	3	3	12.7	12.7	12.7
KIAA0368	KIAA0368	KIAA0368 H	KIAA0368 I	Gene_Sym	IPI001577	IPI001577	3	3	3	>IPI:IPI001	1	3	3	3	1.8	1.8	1.8
#VALUE!	#VALUE!	#VALUE!	#VALUE!	#VALUE!	IPI002985	IPI002985	4	4	4	>IPI:IPI002	1	4	4	4	33.9	33.9	33.9
#VALUE!	#VALUE!	#VALUE!	#VALUE!	#VALUE!	IPI003049	IPI003049	10;10;6;4;4	8;8;4;3;3	2;2;1;0;0	>IPI:IPI003	5	10	8	2	19.3	15.9	3.6
HNRNPK	HNRNPK	HNRNPK Is	HNRNPK Is	Gene_Sym	IPI002167	IPI002167	10;10;10;1	10;10;10;1	10;10;10;1	>IPI:IPI002	7	10	10	10	30	30	30
PKM2	PKM2	PKM2 Isofo	PKM2 Isofo	Gene_Sym	IPI004791	IPI004791	21;19;19;1	21;19;19;1	21;19;19;1	>IPI:IPI004	13	21	21	21	51.4	51.4	51.4
HADHA	HADHA	HADHA Trif	HADHA Tri	Gene_Sym	IPI000315	IPI000315	7;2	7;2	7;2	>IPI:IPI000	2	7	7	7	11	11	11
-	-	cD - cDNA FLJ	- cDNA FLJ	Gene_Sym	IPI009094	IPI009094	2;2;2	2;2;2	2;2;2	>IPI:IPI009	3	2	2	2	11.4	11.4	11.4
RPS2	RPS2	RPS2 40S ri	RPS2 40S r	Gene_Sym	IPI000134	IPI000134	6;6;5;5;4;4	6;6;5;5;4;4	6;6;5;5;4;4	>IPI:IPI000	13	6	6	6	21.2	21.2	21.2
ATAD3B	ATAD3B	ATAD3B Isc	ATAD3B Isc	Gene_Sym	IPI003060	IPI003060	2;2;2;2;2;2	2;2;2;2;2;2	2;2;2;2;2;2	>IPI:IPI003	14	2	2	2	2.9	2.9	2.9

MTHFD1	MTHFD1	MTHFD1 cl	MTHFD1 cl	Gene_Sym	IPI007949(	IPI007949(	18;18	18;18	18;18	>IPI:IPI007	2	18	18	18	19.9	19.9	19.9
DNAJC8	DNAJC8	DNAJC8 Dr	DNAJC8 Dr	Gene_Sym	IPI000034:	IPI000034:	2	2	2	>IPI:IPI000	1	2	2	2	9.5	9.5	9.5
PDLIM1	PDLIM1	PDLIM1 PD	PDLIM1 PD	Gene_Sym	IPI000104:	IPI000104:	3	3	3	>IPI:IPI000	1	3	3	3	16.1	16.1	16.1
HSPB1	HSPB1	HSPB1 Hea	HSPB1 Hea	Gene_Sym	IPI000255:	IPI000255:	4;4;2	4;4;2	4;4;2	>IPI:IPI000	3	4	4	4	25.4	25.4	25.4
PEBP1	PEBP1	PEBP1 Pho	PEBP1 Pho	Gene_Sym	IPI002194(	IPI002194(	7;6;5;3;1	7;6;5;3;1	7;6;5;3;1	>IPI:IPI002	5	7	7	7	47.1	47.1	47.1
RPS3A	RPS3A	RPS3A 40S	RPS3A 40S	Gene_Sym	IPI004198(	IPI004198(	2;2;1;1	2;2;1;1	2;2;1;1	>IPI:IPI004	4	2	2	2	6.4	6.4	6.4
HNRNPH1	HNRNPH1	HNRNPH1	HNRNPH1	Gene_Sym	IPI004791(	IPI004791(	3;3;2;2	3;3;2;2	1;1;1;1	>IPI:IPI004	4	3	3	1	9.3	9.3	3.6
YARS	YARS	YARS Tyros	YARS Tyros	Gene_Sym	IPI000070(	IPI000070(	3	3	3	>IPI:IPI000	1	3	3	3	5.7	5.7	5.7
RPL4	RPL4	RPL4 60S ri	RPL4 60S r	Gene_Sym	IPI000039:	IPI000039:	2;2;1;1;1	2;2;1;1;1	2;2;1;1;1	>IPI:IPI000	5	2	2	2	5.4	5.4	5.4
RPS5	RPS5	RPS5 40S ri	RPS5 40S r	Gene_Sym	IPI000084:	IPI000084:	5;1	5;1	5;1	>IPI:IPI000	2	5	5	5	26	26	26
PSMD9	PSMD9	PSMD9 Iso	PSMD9 Iso	Gene_Sym	IPI000108(	IPI000108(	2;2;2;2	2;2;2;2	2;2;2;2	>IPI:IPI000	4	2	2	2	8.5	8.5	8.5
RPS3	RPS3	RPS3 40S ri	RPS3 40S r	Gene_Sym	IPI000112:	IPI000112:	10;6;4;2	10;6;4;2	10;6;4;2	>IPI:IPI000	4	10	10	10	42.8	42.8	42.8
RBBP7	RBBP7	RBBP7 cDN	RBBP7 cDN	Gene_Sym	IPI006465(	IPI006465(	2;2;2;2;2;2	2;2;2;2;2;2	2;2;2;2;2;2	>IPI:IPI006	12	2	2	2	4.5	4.5	4.5
YWHAH	YWHAH	YWHAH 14	YWHAH 14	Gene_Sym	IPI002163(	IPI002163(	4;1;1	2;1;1	2;1;1	>IPI:IPI002	3	4	2	2	16.7	9.3	9.3
PPA1	PPA1	PPA1 Inorg	PPA1 Inorg	Gene_Sym	IPI000150(	IPI000150(	7;3;2	7;3;2	7;3;2	>IPI:IPI000	3	7	7	7	19.7	19.7	19.7
RPS10	RPS10	RPS10 40S	RPS10 40S	Gene_Sym	IPI000084:	IPI000084:	3;2;2;2;1;1	3;2;2;2;1;1	3;2;2;2;1;1	>IPI:IPI000	6	3	3	3	23	23	23
MSN	MSN	MSN Moes	MSN Moes	Gene_Sym	IPI002193(	IPI002193(	6;6;1	2;2;1	2;2;1	>IPI:IPI002	3	6	2	2	9	3.1	3.1
BUB3	BUB3	BUB3 Mito	BUB3 Mito	Gene_Sym	IPI000134(	IPI000134(	1;1;1	1;1;1	1;1;1	>IPI:IPI000	3	1	1	1	4.3	4.3	4.3
GNB2L1	GNB2L1	GNB2L1 Gu	GNB2L1 Gu	Gene_Sym	IPI008482(	IPI008482(	6;2;2;1	6;2;2;1	6;2;2;1	>IPI:IPI008	4	6	6	6	21.1	21.1	21.1
UCHL5	UCHL5	UCHL5 Ubi	UCHL5 Ubi	Gene_Sym	IPI006423(	IPI006423(	2;2;2;2;2;2	2;2;2;2;2;2	2;2;2;2;2;2	>IPI:IPI006	9	2	2	2	6.8	6.8	6.8
HNRNPR	HNRNPR	HNRNPR 7:	HNRNPR 7	Gene_Sym	IPI009416(	IPI009416(	3;3;3;3;3;2	3;3;3;3;3;2	1;1;1;1;1;1	>IPI:IPI009	6	3	3	1	5.2	5.2	2
C1orf57	C1orf57	C1orf57 Ch	C1orf57 Ch	Gene_Sym	IPI005145(	IPI005145(	3;3	3;3	3;3	>IPI:IPI005	2	3	3	3	19.7	19.7	19.7
MCM6	MCM6	MCM6 DN/	MCM6 DN.	Gene_Sym	IPI000315(	IPI000315(	3	3	3	>IPI:IPI000	1	3	3	3	3.7	3.7	3.7
#VALUE!	#VALUE!	#VALUE!	#VALUE!	#VALUE!	IPI004705(	IPI004705(	2;2;2;2;2;1	2;2;2;2;2;1	2;2;2;2;2;1	>IPI:IPI004	7	2	2	2	7.8	7.8	7.8
FEN1	FEN1	FEN1 Flap	FEN1 Flap	Gene_Sym	IPI000262(	IPI000262(	4	4	4	>IPI:IPI000	1	4	4	4	12.1	12.1	12.1
NAP1L4	NAP1L4	NAP1L4 Pu	NAP1L4 Pu	Gene_Sym	IPI000177(	IPI000177(	4;4;3;3;2;1	3;3;2;2;1;1	3;3;2;2;1;1	>IPI:IPI000	6	4	3	3	13	10.4	10.4
RAD23B	RAD23B	RAD23B U\	RAD23B U\	Gene_Sym	IPI000082(	IPI000082(	3;3;1;1	3;3;1;1	3;3;1;1	>IPI:IPI000	4	3	3	3	6.4	6.4	6.4
#VALUE!	#VALUE!	#VALUE!	#VALUE!	#VALUE!	IPI004143(	IPI004143(	2;2;1	2;2;1	2;2;1	>IPI:IPI004	3	2	2	2	3.3	3.3	3.3
NUDT5	NUDT5	NUDT5 Put	NUDT5 Put	Gene_Sym	IPI006467(	IPI006467(	2;2;1;1;1	2;2;1;1;1	2;2;1;1;1	>IPI:IPI006	5	2	2	2	10.3	10.3	10.3
NAPA	NAPA	NAPA Alph	NAPA Alph	Gene_Sym	IPI000092:	IPI000092:	3	3	3	>IPI:IPI000	1	3	3	3	11.9	11.9	11.9
PPP2R1A	PPP2R1A	PPP2R1A S	PPP2R1A S	Gene_Sym	IPI005547:	IPI005547:	7;7;7;6;6;2	7;7;7;6;6;2	7;7;7;6;6;2	>IPI:IPI005	12	7	7	7	17.3	17.3	17.3
LYPLA1	LYPLA1	LYPLA1 cDI	LYPLA1 cDI	Gene_Sym	IPI000073(	IPI000073(	2;2;2;1	2;2;2;1	2;2;2;1	>IPI:IPI000	4	2	2	2	8	8	8
AIP	AIP	AIP Non-fu	AIP Non-fu	Gene_Sym	IPI009258(	IPI009258(	3;3	3;3	3;3	>IPI:IPI009	2	3	3	3	9.2	9.2	9.2
LONP1	LONP1	LONP1 Lon	LONP1 Lon	Gene_Sym	IPI000051:	IPI000051:	2;2;1	2;2;1	2;2;1	>IPI:IPI000	3	2	2	2	2.3	2.3	2.3
PSMC1	PSMC1	PSMC1 26S	PSMC1 26S	Gene_Sym	IPI000111(	IPI000111(	2;2;2;1	2;2;2;1	2;2;2;1	>IPI:IPI000	4	2	2	2	4.8	4.8	4.8
-	-	29 - 29 kDa pr	- 29 kDa pr	Gene_Sym	IPI004534(	IPI004534(	8;8;3;3;2;1	8;8;3;3;2;1	8;8;3;3;2;1	>IPI:IPI004	8	8	8	8	52.4	52.4	52.4
FKBP4	FKBP4	FKBP4 FK5(	FKBP4 FK5	Gene_Sym	IPI002190(	IPI002190(	7	7	7	>IPI:IPI002	1	7	7	7	18.7	18.7	18.7
SNRPA1	SNRPA1	SNRPA1 U2	SNRPA1 U2	Gene_Sym	IPI002974(	IPI002974(	4;1;1	4;1;1	4;1;1	>IPI:IPI002	3	4	4	4	20.4	20.4	20.4
SFRS2	SFRS2	SFRS2 Splic	SFRS2 Splic	Gene_Sym	IPI000059(	IPI000059(	3;3;3;2;2;2	3;3;3;2;2;2	3;3;3;2;2;2	>IPI:IPI000	9	3	3	3	14.5	14.5	14.5
HNRNPC	HNRNPC	HNRNPC Is	HNRNPC Is	Gene_Sym	IPI004773(	IPI004773(	3;3;3;3;3;3	3;3;3;3;3;3	2;2;2;2;2;2	>IPI:IPI004	10	3	3	2	12.7	12.7	8.8
ARHGDIA	ARHGDIA	ARHGDIA 2	ARHGDIA 2	Gene_Sym	IPI007944(	IPI007944(	4;4;4;4;3;3	4;4;4;4;3;3	4;4;4;4;3;3	>IPI:IPI007	7	4	4	4	15.7	15.7	15.7

KHSRP	KHSRP	KHSRP KH-	KHSRP KH-	Gene_Sym	IPI004797	IPI004797	12;12;6	12;12;6	10;10;6	>IPI:IPI004	3	12	12	10	21.5	21.5	19.3
PGLS	PGLS	PGLS 6-phc	PGLS 6-phc	Gene_Sym	IPI000299	IPI000299	4;1	4;1	4;1	>IPI:IPI000	2	4	4	4	18.2	18.2	18.2
OTUB1	OTUB1	OTUB1 cDI	OTUB1 cDI	Gene_Sym	IPI000005	IPI000005	6;6;3	6;6;3	6;6;3	>IPI:IPI000	3	6	6	6	23.4	23.4	23.4
DDOST	DDOST	DDOST Dol	DDOST Dol	Gene_Sym	IPI002970	IPI002970	3;2	3;2	3;2	>IPI:IPI002	2	3	3	3	6.8	6.8	6.8
#VALUE!	#VALUE!	#VALUE!	#VALUE!	#VALUE!	IPI002210	IPI002210	5;4;4;4;4;3	5;4;4;4;4;3	5;4;4;4;4;3	>IPI:IPI002	9	5	5	5	22.2	22.2	22.2
RAC2	RAC2	RAC2 Ras-r	RAC2 Ras-r	Gene_Sym	IPI000102	IPI000102	4;4;4;3;3;3	4;4;4;3;3;3	4;4;4;3;3;3	>IPI:IPI000	8	4	4	4	22.9	22.9	22.9
HNRNPD	HNRNPD	HNRNPD Is	HNRNPD Is	Gene_Sym	IPI000288	IPI000288	4;4;4;4;4;4	4;4;4;4;4;4	3;3;3;3;3;3	>IPI:IPI000	6	4	4	3	11.3	11.3	9
GRPEL1	GRPEL1	GRPEL1 Gr	GRPEL1 Gr	Gene_Sym	IPI000295	IPI000295	3;3	3;3	3;3	>IPI:IPI000	2	3	3	3	14.3	14.3	14.3
STMN1	STMN1	STMN1 sta	STMN1 sta	Gene_Sym	IPI009219	IPI009219	4;4;4;4;3	4;4;4;4;3	2;2;2;2;1	>IPI:IPI009	5	4	4	2	21.3	21.3	11.5
ANP32B	ANP32B	ANP32B Isc	ANP32B Isc	Gene_Sym	IPI000074	IPI000074	4;4;3	2;2;1	2;2;1	>IPI:IPI000	3	4	2	2	21.1	9.6	9.6
RPS4X	RPS4X	RPS4X 40S	RPS4X 40S	Gene_Sym	IPI002170	IPI002170	5;2;2;2;1;1	5;2;2;2;1;1	5;2;2;2;1;1	>IPI:IPI002	8	5	5	5	18.6	18.6	18.6
GANAB	GANAB	GANAB cDI	GANAB cD	Gene_Sym	IPI003835	IPI003835	4;4;4;1	4;4;4;1	4;4;4;1	>IPI:IPI003	4	4	4	4	4.1	4.1	4.1
NAT13	NAT13	NAT13 Isof	NAT13 Isof	Gene_Sym	IPI000186	IPI000186	4;4;4;3;3;2	4;4;4;3;3;2	4;4;4;3;3;2	>IPI:IPI000	9	4	4	4	27.2	27.2	27.2
TMPO	TMPO	TMPO Lam	TMPO Lam	Gene_Sym	IPI002162	IPI002162	6	6	2	>IPI:IPI002	1	6	6	2	11.2	11.2	3
ACP1	ACP1	ACP1 Isofo	ACP1 Isofo	Gene_Sym	IPI002198	IPI002198	4;3;3;2;2;2	4;3;3;2;2;2	4;3;3;2;2;2	>IPI:IPI002	10	4	4	4	31.6	31.6	31.6
HDGF	HDGF	HDGF Hepa	HDGF Hepa	Gene_Sym	IPI000209	IPI000209	3;2;2;2	3;2;2;2	3;2;2;2	>IPI:IPI000	4	3	3	3	14.2	14.2	14.2
-	-	66 - 66 kDa pr	- 66 kDa pr	Gene_Sym	IPI009419	IPI009419	10;10;10;1	10;10;10;1	10;10;10;1	>IPI:IPI009	11	10	10	10	20.2	20.2	20.2
IGK@	IGK@	IGK@ IGK(	IGK@ IGK(	Gene_Sym	IPI007848	IPI007848	5;4;4;4;4;4	1;0;0;0;0;0	0;0;0;0;0;0	>IPI:IPI007	15	5	1	0	33.9	3.8	0
-	-	An - Anti-(ED-I	- Anti-(ED-I	Gene_Sym	IPI009164	IPI009164	4;4;4;4;4;3	2;2;2;2;2;1	2;2;2;2;2;1	>IPI:IPI009	16	4	2	2	27.3	16.8	16.8
ARL3	ARL3	ARL3 ADP-I	ARL3 ADP-	Gene_Sym	IPI000033	IPI000033	4	4	4	>IPI:IPI000	1	4	4	4	34.1	34.1	34.1
PLIN3	PLIN3	PLIN3 Isofc	PLIN3 Isofc	Gene_Sym	IPI003038	IPI003038	4;4;4	4;4;4	4;4;4	>IPI:IPI003	3	4	4	4	14.3	14.3	14.3
PRDX2	PRDX2	PRDX2 Per	PRDX2 Per	Gene_Sym	IPI000273	IPI000273	10;10;7;3	10;10;7;3	9;9;7;3	>IPI:IPI000	4	10	10	9	38.9	38.9	33.3
-	-	Ig l - Ig heavy c	- Ig heavy c	Gene_Sym	IPI003855	IPI003855	1;1	1;1	1;1	>IPI:IPI003	2	1	1	1	4.8	4.8	4.8
MCM5	MCM5	MCM5 DNA	MCM5 DN	Gene_Sym	IPI000183	IPI000183	2;2;2;2;1;1	2;2;2;2;1;1	2;2;2;2;1;1	>IPI:IPI000	8	2	2	2	3.4	3.4	3.4
SF3A1	SF3A1	SF3A1 Splic	SF3A1 Splic	Gene_Sym	IPI000174	IPI000174	2	2	2	>IPI:IPI000	1	2	2	2	2.6	2.6	2.6
ANXA2	ANXA2	ANXA2 Isof	ANXA2 Isof	Gene_Sym	IPI004181	IPI004181	10;10;8;8;7	10;10;8;8;7	10;10;8;8;7	>IPI:IPI004	8	10	10	10	33.3	33.3	33.3
MDH1	MDH1	MDH1 Mal	MDH1 Mal	Gene_Sym	IPI009161	IPI009161	7;6;5;3;2;1	7;6;5;3;2;1	7;6;5;3;2;1	>IPI:IPI009	6	7	7	7	26.1	26.1	26.1
RAB11A	RAB11A	RAB11A cD	RAB11A cD	Gene_Sym	IPI004291	IPI004291	4;4;4;4;4;1	4;4;4;4;4;1	4;4;4;4;4;1	>IPI:IPI004	7	4	4	4	16.1	16.1	16.1
EIF3L	EIF3L	EIF3L Euka	EIF3L Euka	Gene_Sym	IPI004652	IPI004652	4;4;4;4;2;2	4;4;4;4;2;2	4;4;4;4;2;2	>IPI:IPI004	6	4	4	4	7.6	7.6	7.6
FKBP3	FKBP3	FKBP3 FK5	FKBP3 FK5	Gene_Sym	IPI000241	IPI000241	3	3	3	>IPI:IPI000	1	3	3	3	13.4	13.4	13.4
PHGDH	PHGDH	PHGDH D-3	PHGDH D-3	Gene_Sym	IPI000112	IPI000112	7;6	7;6	7;6	>IPI:IPI000	2	7	7	7	15.4	15.4	15.4
SEPT7	SEPT7	SEPT7 Isof	SEPT7 Isof	Gene_Sym	IPI009415	IPI009415	2;2;2;1;1;1	2;2;2;1;1;1	2;2;2;1;1;1	>IPI:IPI009	7	2	2	2	5.9	5.9	5.9
PPIA	PPIA	PPIA Peptic	PPIA Peptic	Gene_Sym	IPI004195	IPI004195	12;10;8;6;6	12;10;8;6;6	12;10;8;6;6	>IPI:IPI004	18	12	12	12	58.2	58.2	58.2
GLRX3	GLRX3	GLRX3 Glut	GLRX3 Glu	Gene_Sym	IPI000085	IPI000085	3	3	3	>IPI:IPI000	1	3	3	3	10.1	10.1	10.1
PAICS	PAICS	PAICS Mult	PAICS Mult	Gene_Sym	IPI002172	IPI002172	12;11	12;11	12;11	>IPI:IPI002	2	12	12	12	28.6	28.6	28.6
VAPA	VAPA	VAPA vesic	VAPA vesic	Gene_Sym	IPI003746	IPI003746	3;3;3;2;1;1	3;3;3;2;1;1	3;3;3;2;1;1	>IPI:IPI003	6	3	3	3	9.5	9.5	9.5
USP5	USP5	USP5 Isofo	USP5 Isofo	Gene_Sym	IPI000246	IPI000246	4;4	4;4	4;4	>IPI:IPI000	2	4	4	4	4.9	4.9	4.9
PSMD1	PSMD1	PSMD1 Isof	PSMD1 Iso	Gene_Sym	IPI002996	IPI002996	2;2	2;2	2;2	>IPI:IPI002	2	2	2	2	2.8	2.8	2.8
PCBP1	PCBP1	PCBP1 Poly	PCBP1 Poly	Gene_Sym	IPI000166	IPI000166	7	7	5	>IPI:IPI000	1	7	7	5	26.4	26.4	17.7
#VALUE!	#VALUE!	LOC72397	LOC72397	Gene_Sym	IPI000258	IPI000258	5;5;5;2;2;1	5;5;5;2;2;1	3;3;3;1;2;1	>IPI:IPI000	7	5	5	3	22.9	22.9	11.2
PTMA;PTM	PTMA;PTM	PTMA;PTM	PTMA;PTM	Gene_Sym	IPI009172	IPI009172	2;2;2;2;2;2	2;2;2;2;2;2	2;2;2;2;2;2	>IPI:IPI009	13	2	2	2	7.4	7.4	7.4

#VALUE!	#VALUE!	#VALUE!	#VALUE!	#VALUE!	IPI005500(	IPI005500(	3	3	3	>IPI:IPI005	1	3	3	3	8.9	8.9	8.9
SRM	SRM	SRM Sperm	SRM Sperm	Gene_Sym	IPI0029202	IPI0029202	4	4	4	>IPI:IPI002	1	4	4	4	12.9	12.9	12.9
SH3BGRL3	SH3BGRL3	SH3BGRL3	SH3BGRL3	Gene_Sym	IPI000104(	IPI000104(	1;1;1	1;1;1	1;1;1	>IPI:IPI000	3	1	1	1	4.4	4.4	4.4
GRHPR	GRHPR	GRHPR GR	GRHPR GR	Gene_Sym	IPI005506(	IPI005506(	2;2;1	2;2;1	2;2;1	>IPI:IPI005	3	2	2	2	7.9	7.9	7.9
MCM3	MCM3	MCM3 MC	MCM3 MC	Gene_Sym	IPI000132	IPI000132	3;3	3;3	3;3	>IPI:IPI000	2	3	3	3	3.8	3.8	3.8
PCBP2	PCBP2	PCBP2 poly	PCBP2 poly	Gene_Sym	IPI007963	IPI007963	6;6;6;6;6;6	4;4;4;4;4;4	4;4;4;4;4;4	>IPI:IPI007	19	6	4	4	23.2	14.8	14.8
STIP1	STIP1	STIP1 Stres	STIP1 Stres	Gene_Sym	IPI000138	IPI000138	17;15;14	17;15;14	17;15;14	>IPI:IPI000	3	17	17	17	32	32	32
YWHAQ	YWHAQ	YWHAQ 14	YWHAQ 14	Gene_Sym	IPI000181	IPI000181	9;4	6;3	6;3	>IPI:IPI000	2	9	6	6	42	31	31
THOP1	THOP1	THOP1 Thi	THOP1 Thi	Gene_Sym	IPI005491	IPI005491	3;1	3;1	3;1	>IPI:IPI005	2	3	3	3	4.8	4.8	4.8
HNRNPA1	HNRNPA1	HNRNPA1 I	HNRNPA1	Gene_Sym	IPI002159	IPI002159	2;2;2;2;2;1	2;2;2;2;2;1	2;2;2;2;2;1	>IPI:IPI002	13	2	2	2	7	7	7
NAPG	NAPG	NAPG Gam	NAPG Gam	Gene_Sym	IPI002938	IPI002938	2;2	2;2	2;2	>IPI:IPI002	2	2	2	2	7.4	7.4	7.4
TPM3	TPM3	TPM3 Isofo	TPM3 Isofo	Gene_Sym	IPI002183	IPI002183	4;4;4;3;3;3	4;4;4;3;3;3	4;4;4;3;3;3	>IPI:IPI002	38	4	4	4	17.3	17.3	17.3
CNN2	CNN2	CNN2 cDN	CNN2 cDN	Gene_Sym	IPI009105	IPI009105	3;3;2;1;1;1	3;3;2;1;1;1	3;3;2;1;1;1	>IPI:IPI009	6	3	3	3	11.8	11.8	11.8
-	-	52 - 52 kDa pr	- 52 kDa pr	Gene_Sym	IPI007957	IPI007957	3;3;2;2;2	3;3;2;2;2	3;3;2;2;2	>IPI:IPI007	5	3	3	3	6.3	6.3	6.3
MAGOHB	MAGOHB	MAGOHB F	MAGOHB F	Gene_Sym	IPI000592	IPI000592	2;2;2;1;1;1	2;2;2;1;1;1	2;2;2;1;1;1	>IPI:IPI000	7	2	2	2	20.9	20.9	20.9
API5	API5	API5 apopt	API5 apopt	Gene_Sym	IPI008558	IPI008558	3;3;3;3;2;2	3;3;3;3;2;2	3;3;3;3;2;2	>IPI:IPI008	6	3	3	3	8	8	8
IGKV3-20	IGKV3-20	IGKV3-20 I	IGKV3-20 I	Gene_Sym	IPI008891	IPI008891	5;5	5;5	0;0	>IPI:IPI008	2	5	5	0	36.9	36.9	0
PSMB6	PSMB6	PSMB6 Pro	PSMB6 Pro	Gene_Sym	IPI000008	IPI000008	3;3;2	3;3;2	3;3;2	>IPI:IPI000	3	3	3	3	13	13	13
KHDRBS1	KHDRBS1	KHDRBS1 I	KHDRBS1 I	Gene_Sym	IPI000085	IPI000085	1;1;1	1;1;1	1;1;1	>IPI:IPI000	3	1	1	1	2.3	2.3	2.3
DTYMK	DTYMK	DTYMK Thy	DTYMK Thy	Gene_Sym	IPI000138	IPI000138	3;3;1	3;3;1	3;3;1	>IPI:IPI000	3	3	3	3	14.6	14.6	14.6
TOMM34	TOMM34	TOMM34 M	TOMM34 M	Gene_Sym	IPI000099	IPI000099	2;1	2;1	2;1	>IPI:IPI000	2	2	2	2	8.7	8.7	8.7
CDC37	CDC37	CDC37 Hsp	CDC37 Hsp	Gene_Sym	IPI000131	IPI000131	2	2	2	>IPI:IPI000	1	2	2	2	7.9	7.9	7.9
PPM1G	PPM1G	PPM1G Pro	PPM1G Pro	Gene_Sym	IPI000061	IPI000061	2;1	2;1	2;1	>IPI:IPI000	2	2	2	2	4.2	4.2	4.2
ELAVL1	ELAVL1	ELAVL1 cDI	ELAVL1 cD	Gene_Sym	IPI003019	IPI003019	3;3	3;3	3;3	>IPI:IPI003	2	3	3	3	9.9	9.9	9.9
PRKCSH	PRKCSH	PRKCSH cD	PRKCSH cD	Gene_Sym	IPI000261	IPI000261	2;2;2;2	2;2;2;2	2;2;2;2	>IPI:IPI000	4	2	2	2	3.9	3.9	3.9
SNRPA	SNRPA	SNRPA U1	SNRPA U1	Gene_Sym	IPI000123	IPI000123	2;1	2;1	2;1	>IPI:IPI000	2	2	2	2	6.4	6.4	6.4
PPAT	PPAT	PPAT Amid	PPAT Amid	Gene_Sym	IPI000295	IPI000295	2;1	2;1	2;1	>IPI:IPI000	2	2	2	2	4.3	4.3	4.3
FUS	FUS	FUS Fus-lik	FUS Fus-lik	Gene_Sym	IPI002607	IPI002607	3;3;3;3;3;3	3;3;3;3;3;3	3;3;3;3;3;3	>IPI:IPI002	9	3	3	3	6.2	6.2	6.2
AKR1A1	AKR1A1	AKR1A1 Al	AKR1A1 Al	Gene_Sym	IPI002202	IPI002202	3	3	3	>IPI:IPI002	1	3	3	3	10.8	10.8	10.8
HPRT1	HPRT1	HPRT1 Hyp	HPRT1 Hyp	Gene_Sym	IPI002184	IPI002184	3;2	3;2	3;2	>IPI:IPI002	2	3	3	3	16.5	16.5	16.5
SFRS3	SFRS3	SFRS3 Splic	SFRS3 Splic	Gene_Sym	IPI000102	IPI000102	3;3	3;3	2;2	>IPI:IPI000	2	3	3	2	18.3	18.3	18.3
GMFG	GMFG	GMFG Glia	GMFG Glia	Gene_Sym	IPI000284	IPI000284	3;1;1	3;1;1	3;1;1	>IPI:IPI000	3	3	3	3	20.4	20.4	20.4
SNRNP70	SNRNP70	SNRNP70 I	SNRNP70 I	Gene_Sym	IPI002902	IPI002902	2;2;1;1	2;2;1;1	2;2;1;1	>IPI:IPI002	4	2	2	2	4.1	4.1	4.1
BAT1	BAT1	BAT1 Isofo	BAT1 Isofo	Gene_Sym	IPI006418	IPI006418	3;3;3;2;2;2	3;3;3;2;2;2	3;3;3;2;2;2	>IPI:IPI006	28	3	3	3	7.4	7.4	7.4
SOD1	SOD1	SOD1 Supe	SOD1 Supe	Gene_Sym	IPI002187	IPI002187	3;2	3;2	3;2	>IPI:IPI002	2	3	3	3	21.4	21.4	21.4
CORO1A	CORO1A	CORO1A C	CORO1A C	Gene_Sym	IPI000101	IPI000101	1;1	1;1	1;1	>IPI:IPI000	2	1	1	1	2.2	2.2	2.2
DNAJC9	DNAJC9	DNAJC9 Dn	DNAJC9 Dn	Gene_Sym	IPI001549	IPI001549	4;1	4;1	4;1	>IPI:IPI001	2	4	4	4	18.8	18.8	18.8
DPP3	DPP3	DPP3 Isofo	DPP3 Isofo	Gene_Sym	IPI000206	IPI000206	3;1	3;1	3;1	>IPI:IPI000	2	3	3	3	5.8	5.8	5.8
CTBP1	CTBP1	CTBP1 C-te	CTBP1 C-te	Gene_Sym	IPI000128	IPI000128	2;2	2;2	2;2	>IPI:IPI000	2	2	2	2	4.8	4.8	4.8
PSMD13	PSMD13	PSMD13 pr	PSMD13 pr	Gene_Sym	IPI003753	IPI003753	4;4	4;4	4;4	>IPI:IPI003	2	4	4	4	11.6	11.6	11.6
HNRNPM	HNRNPM	HNRNPM I	HNRNPM I	Gene_Sym	IPI001719	IPI001719	2;2	2;2	2;2	>IPI:IPI001	2	2	2	2	2.9	2.9	2.9

DRG1	DRG1	DRG1 Deve	DRG1 Deve	Gene_Sym	IPI000318	IPI000318	2;2	2;2	2;2	>IPI:IPI000	2	2	2	2	6.8	6.8	6.8
DAP3	DAP3	DAP3 28S r	DAP3 28S r	Gene_Sym	IPI000181	IPI000181	2;2	2;2	2;2	>IPI:IPI000	2	2	2	2	6.5	6.5	6.5
TRIM28	TRIM28	TRIM28 Isc	TRIM28 Isc	Gene_Sym	IPI004382	IPI004382	2;2	2;2	2;2	>IPI:IPI004	2	2	2	2	3.8	3.8	3.8
TXNL1	TXNL1	TXNL1 cDN	TXNL1 cDN	Gene_Sym	IPI006420	IPI006420	3;3	3;3	3;3	>IPI:IPI006	2	3	3	3	13.8	13.8	13.8
ACAT1	ACAT1	ACAT1 Ace	ACAT1 Ace	Gene_Sym	IPI000303	IPI000303	8;4	8;4	8;4	>IPI:IPI000	2	8	8	8	25.5	25.5	25.5
SIRT3	SIRT3	SIRT3 cDN	SIRT3 cDN	Gene_Sym	IPI001831	IPI001831	2;2;1;1	2;2;1;1	2;2;1;1	>IPI:IPI001	4	2	2	2	5.3	5.3	5.3
PAFAH1B3	PAFAH1B3	PAFAH1B3	PAFAH1B3	Gene_Sym	IPI000148	IPI000148	2	2	2	>IPI:IPI000	1	2	2	2	7.8	7.8	7.8
HNRNPU	HNRNPU	HNRNPU Is	HNRNPU Is	Gene_Sym	IPI008838	IPI008838	5;5;5;5;4	5;5;5;5;4	5;5;5;5;4	>IPI:IPI008	5	5	5	5	8.5	8.5	8.5
ADRM1	ADRM1	ADRM1 Pro	ADRM1 Pro	Gene_Sym	IPI000330	IPI000330	1;1	1;1	1;1	>IPI:IPI000	2	1	1	1	3.9	3.9	3.9
MTAP	MTAP	MTAP cDN	MTAP cDN	Gene_Sym	IPI000118	IPI000118	1;1;1;1;1	1;1;1;1;1	1;1;1;1;1	>IPI:IPI000	5	1	1	1	6	6	6
G6PD	G6PD	G6PD Isofo	G6PD Isofo	Gene_Sym	IPI002160	IPI002160	2;2;2;2;1;1	2;2;2;2;1;1	2;2;2;2;1;1	>IPI:IPI002	6	2	2	2	4.5	4.5	4.5
GOT1	GOT1	GOT1 Aspa	GOT1 Aspa	Gene_Sym	IPI002190	IPI002190	8;7	8;7	8;7	>IPI:IPI002	2	8	8	8	24.5	24.5	24.5
SET	SET	SET Isoforn	SET Isoforr	Gene_Sym	IPI000723	IPI000723	4;4;4;4;4;3	4;4;4;4;4;3	4;4;4;4;4;3	>IPI:IPI000	10	4	4	4	16.6	16.6	16.6
TUBA4A	TUBA4A	TUBA4A Tu	TUBA4A Tu	Gene_Sym	IPI000077	IPI000077	14;14;7;5;5	3;3;3;3;3;0	3;3;3;3;3;0	>IPI:IPI000	14	14	3	3	42.6	9.8	9.8
CPNE1	CPNE1	CPNE1 cop	CPNE1 cop	Gene_Sym	IPI008944	IPI008944	3;3;3;2;1;1	3;3;3;2;1;1	3;3;3;2;1;1	>IPI:IPI008	14	3	3	3	7	7	7
HNRNPH3	HNRNPH3	HNRNPH3	HNRNPH3	Gene_Sym	IPI000138	IPI000138	2;2;2;1;1;1	2;2;2;1;1;1	2;2;2;1;1;1	>IPI:IPI000	7	2	2	2	8.4	8.4	8.4
ACTR1A	ACTR1A	ACTR1A Al	ACTR1A Al	Gene_Sym	IPI000294	IPI000294	4;4;1;1	4;4;1;1	4;4;1;1	>IPI:IPI000	4	4	4	4	17.3	17.3	17.3
CBR1	CBR1	CBR1 Carb	CBR1 Carb	Gene_Sym	IPI002953	IPI002953	2;2;2;1	2;2;2;1	2;2;2;1	>IPI:IPI002	4	2	2	2	11.9	11.9	11.9
HNRNPA2E	HNRNPA2E	HNRNPA2E	HNRNPA2E	Gene_Sym	IPI003963	IPI003963	5;5;4	5;5;4	5;5;4	>IPI:IPI003	3	5	5	5	13.3	13.3	13.3
ALDOC	ALDOC	ALDOC Fru	ALDOC Fru	Gene_Sym	IPI004182	IPI004182	3;3;2;1	2;2;1;1	2;2;1;1	>IPI:IPI004	4	3	2	2	10.2	8.6	8.6
AKR7A2	AKR7A2	AKR7A2 Af	AKR7A2 Af	Gene_Sym	IPI003059	IPI003059	2;2;2;1;1	2;2;2;1;1	2;2;2;1;1	>IPI:IPI003	5	2	2	2	9.5	9.5	9.5
PRKACA	PRKACA	PRKACA Isc	PRKACA Isc	Gene_Sym	IPI003966	IPI003966	2;2;1;1;1;1	2;2;1;1;1;1	2;2;1;1;1;1	>IPI:IPI003	12	2	2	2	6	6	6
PSMC6	PSMC6	PSMC6 pro	PSMC6 prc	Gene_Sym	IPI009269	IPI009269	3;3;2;1	3;3;2;1	3;3;2;1	>IPI:IPI009	4	3	3	3	9.9	9.9	9.9
AHSA1	AHSA1	AHSA1 Acti	AHSA1 Act	Gene_Sym	IPI000307	IPI000307	3	3	3	>IPI:IPI000	1	3	3	3	9.2	9.2	9.2
TSN	TSN	TSN Transli	TSN Transl	Gene_Sym	IPI000187	IPI000187	4;4;4;2	4;4;4;2	4;4;4;2	>IPI:IPI000	4	4	4	4	19.7	19.7	19.7
ALDOA	ALDOA	ALDOA 45	ALDOA 45	Gene_Sym	IPI007963	IPI007963	16;16;1;1;1	16;16;1;1;1	15;15;0;0;0	>IPI:IPI007	6	16	16	15	44.5	44.5	42.8
EIF3G	EIF3G	EIF3G Euka	EIF3G Euka	Gene_Sym	IPI002904	IPI002904	3;1	3;1	3;1	>IPI:IPI002	2	3	3	3	11.2	11.2	11.2
ATIC	ATIC	ATIC Bifun	ATIC Bifun	Gene_Sym	IPI002894	IPI002894	16;15;6;5;3	16;15;6;5;3	16;15;6;5;3	>IPI:IPI002	7	16	16	16	35.6	35.6	35.6
SFRS7	SFRS7	SFRS7 Isof	SFRS7 Isof	Gene_Sym	IPI000033	IPI000033	3;3;3;3;2;1	2;2;2;2;2;1	2;2;2;2;2;1	>IPI:IPI000	6	3	2	2	14.7	8.8	8.8
NUDC	NUDC	NUDC Nucl	NUDC Nuc	Gene_Sym	IPI005507	IPI005507	5;5;3;1	5;5;3;1	5;5;3;1	>IPI:IPI005	4	5	5	5	15.7	15.7	15.7
THOC4	THOC4	THOC4 TH	THOC4 TH	Gene_Sym	IPI003288	IPI003288	2	2	2	>IPI:IPI003	1	2	2	2	11	11	11
ILF2	ILF2	ILF2 Interle	ILF2 Interle	Gene_Sym	IPI000051	IPI000051	6;2;2	6;2;2	6;2;2	>IPI:IPI000	3	6	6	6	20.3	20.3	20.3
NCL	NCL	NCL Nuclec	NCL Nuclec	Gene_Sym	IPI006046	IPI006046	20;18;12;1	20;18;12;1	20;18;12;1	>IPI:IPI006	7	20	20	20	28.5	28.5	28.5
XRCC6	XRCC6	XRCC6 AT	XRCC6 AT	Gene_Sym	IPI006447	IPI006447	4;4;3;3	4;4;3;3	4;4;3;3	>IPI:IPI006	4	4	4	4	8.2	8.2	8.2
GGCT	GGCT	GGCT Isofo	GGCT Isofo	Gene_Sym	IPI000315	IPI000315	3;2;2;1;1	3;2;2;1;1	3;2;2;1;1	>IPI:IPI000	5	3	3	3	17.6	17.6	17.6
SFRS1	SFRS1	SFRS1 Isof	SFRS1 Isof	Gene_Sym	IPI002185	IPI002185	4;4;4;1	4;4;4;1	4;4;4;1	>IPI:IPI002	4	4	4	4	14	14	14
HNRNPAB	HNRNPAB	HNRNPAB	HNRNPAB	Gene_Sym	IPI003345	IPI003345	2;2;2;1;1	2;2;2;1;1	2;2;2;1;1	>IPI:IPI003	5	2	2	2	6.6	6.6	6.6
SEPT9	SEPT9	SEPT9 sept	SEPT9 sept	Gene_Sym	IPI007846	IPI007846	7;7;7;7;7;7	7;7;7;7;7;7	7;7;7;7;7;7	>IPI:IPI007	8	7	7	7	13.7	13.7	13.7
RRM2	RRM2	RRM2 ribo	RRM2 ribo	Gene_Sym	IPI000111	IPI000111	2;2	2;2	2;2	>IPI:IPI000	2	2	2	2	5.8	5.8	5.8
HIST1H1B	HIST1H1B	HIST1H1B I	HIST1H1B	Gene_Sym	IPI002174	IPI002174	3	3	3	>IPI:IPI002	1	3	3	3	10.6	10.6	10.6
HIST1H1D	HIST1H1D	HIST1H1D I	HIST1H1D	Gene_Sym	IPI002174	IPI002174	5;5;5;1;1	5;5;5;1;1	5;5;5;1;1	>IPI:IPI002	5	5	5	5	15.4	15.4	15.4

XRCC5	XRCC5	XRCC5 ATP	XRCC5 ATP	Gene_Sym	IPI002208	IPI002208	5;1	5;1	5;1	>IPI:IPI002	2	5	5	5	6.6	6.6	6.6
#VALUE!	#VALUE!	#VALUE!	#VALUE!	#VALUE!	IPI000057	IPI000057	2;2;2;2	2;2;2;2	2;2;2;2	>IPI:IPI000	4	2	2	2	5.8	5.8	5.8
SEPT2	SEPT2	SEPT2 Isof	SEPT2 Isof	Gene_Sym	IPI008718	IPI008718	3;3;3;3;3;3	3;3;3;3;3;3	3;3;3;3;3;3	>IPI:IPI008	16	3	3	3	10.6	10.6	10.6
#VALUE!	#VALUE!	IGL@;IGLV	IGL@;IGLV	Gene_Sym	IPI007888	IPI007888	2;2;2;2;2;2	2;2;2;2;2;2	2;2;2;2;2;2	>IPI:IPI007	24	2	2	2	8.7	8.7	8.7

d on log2 Heavy/Light ratio. Proteins highlghted in pink significantly decreased upon stimulation (log2H/L≤-0.5)(17 proteins). Proteins highlighted in green significantly increased upon stimulation (log2H/L≥0.5

Mol. weigh	Sequence l	Sequence l	PEP	Ratio H/L	Ratio H/L n	log2	Ratio H/L v	Ratio H/L c	Intensity	Intensity L	Intensity H	id	Peptide IDs	Peptide is r	Mod. pepti	Evidence ID
72.065	635	635;612;33	5.63E-28	6.9435	8.7419	3.127947	42.915	8	19445000	1947200	17498000	294	664;1169;1	True;True;	664;1169;1	1044;1818
53.651	466	466;173;47	3.36E-140	5.5216	7.0128	2.809991	58.429	31	110920000	18341000	92578000	786	456;538;65	True;True;	456;538;65	749;855;10
26.119	230	230;229;20	1.34E-28	4.6218	5.7851	2.532342	25.648	7	10612000	1826300	8785600	436	879;2315;3	True;True;	879;2315;3	1371;1372
66.408	586	586;387	4.54E-127	2.9733	3.5289	1.819219	18.497	30	124770000	31380000	93385000	587	111;245;24	True;True;	111;245;24	191;192;19
69.948	620	620;600	3.10E-11	2.2721	2.6239	1.391713	21.141	5	9783600	3172900	6610700	159	110;1104;1	True;True;	110;1104;1	190;1742;2
133.29	1189	1189;1188	0.004398	1.5215	1.8917	0.919683	62.544	2	1206900	556590	650360	736	915;2814	True;True	915;2815	1428;4428
53.983	486	486;449	5.99E-08	1.3302	1.6747	0.743903	13.848	3	6240100	2649500	3590600	400	1055;2883	True;True	1055;2884	1670;1671
8.7813	75	75	0.007625	1.1998	1.6709	0.740625	20.813	3	1815600	864560	951040	255	113;369	True;True	113;369	195;196;61
71.223	640	640	4.20E-05	1.3328	1.6415	0.715015	71.577	2	2163400	756820	1406600	360	804;3225	True;True	804;3226	1265;5109
48.115	417	417;374	1.26E-13	1.4504	1.6115	0.688404	18.666	2	5556000	2202700	3353300	320	1735	TRUE	1735	2722;2723
10.932	102	102;101;47	5.00E-31	1.1486	1.5996	0.677711	1.7873	4	16219000	7497000	8722300	631	1068;3109	True;True;	1068;3110	1689;4911
57.293	520	520	3.30E-19	1.2661	1.58	0.659925	6.4517	2	2459000	1091800	1367200	144	1912;3219	True;True;	1912;3220	3013;5099
125.54	1115	1115;1097	3.38E-07	1.2563	1.5644	0.645609	5.7839	3	1583100	650950	932130	875	1524;2051	True;True;	1524;2051	2396;3196
47.46	429	429;387;42	2.08E-07	1.2112	1.5628	0.644133	69.307	2	5337700	2308700	3029000	73	1779;2696	True;True	1779;2697	2805;4224
42.051	377	377;377;34	4.59E-80	1.2201	1.5215	0.605494	19.872	7	90850000	39694000	51157000	331	106;338;52	False;False	106;338;52	176;177;17
191.61	1675	1675;1639	9.77E-82	1.1736	1.5066	0.591296	7.8769	15	17680000	8225800	9454100	367	1159;1663	True;True;	1159;1663	1808;2618
42.003	376	376	9.55E-53	1.1797	1.4847	0.570171	2.0289	6	69204000	31412000	37792000	64	526;1268;1	False;False	526;1268;1	833;834;83
18.041	166	166;166;13	1.52E-05	1.0863	1.4346	0.520649	17.61	4	43518000	21198000	22320000	293	807;1857;2	True;True;	807;1857;2	1268;2925
32.895	298	298	4.08E-32	1.1732	1.4266	0.512581	7.5977	14	37524000	17501000	20023000	124	34;437;786	True;True;	34;437;786	52;724;725
47.371	418	418;418;34	8.40E-54	1.0923	1.4068	0.492417	8.0695	6	20569000	9340400	11229000	439	480;925;11	True;True;	480;925;11	781;1454;1
11.749	105	105;101;10	5.16E-14	1.0544	1.4049	0.490467	6.3437	5	8624500	4153900	4470600	812	44;45;2742	True;True;	44;45;2743	72;73;4290
125.14	1145	1145;1101	1.36E-09	1.1052	1.4032	0.488721	3.3742	2	1254600	602600	651980	328	461;2756	True;True	461;2757	755;4316
21.588	187	187;181;16	4.64E-14	1.0979	1.4023	0.487795	3.4196	7	17397000	8461000	8936200	837	71;748;154	True;True;	71;748;154	118;119;11
14.095	130	130;130;13	8.10E-15	1.0102	1.3904	0.4755	47.26	7	31143000	14788000	16355000	502	118;2148;3	True;True;	118;2148;3	201;202;20
29.212	258	258;249;22	6.47E-14	1.0731	1.3824	0.467175	13.692	6	15583000	7347500	8235900	854	321;353;87	True;True;	321;353;87	542;595;59
30.112	266	266;296;22	4.90E-48	1.1155	1.3748	0.459222	12.504	12	56270000	26325000	29945000	884	875;1078;1	True;True;	875;1078;1	1365;1366
11.428	103	103	2.31E-10	0.98298	1.369	0.453122	11.703	3	2858200	1383600	1474600	429	1558;1670	True;True;	1558;1670	2438;2631
54.636	510	510;467	8.15E-52	1.0656	1.3667	0.450697	3.706	4	13735000	6623900	7111400	687	1;141;1337	True;True;	1;141;1337	1;233;2092
15.278	135	135	2.45E-05	1.0196	1.3529	0.436055	24.344	2	2929900	1235500	1694400	528	1932;3184	True;True	1932;3185	3044;3045
28.607	254	254;254;22	2.33E-43	1.0935	1.3445	0.42707	15.164	8	29931000	14234000	15696000	97	863;2991	True;True	863;2992	1337;1338
57.41	509	509;469;50	6.44E-09	1.0559	1.3398	0.422018	34.588	3	3415900	1608500	1807400	338	291;547;33	True;True;	291;547;33	502;867;52
34.333	300	300;200;16	0.001204	1.1353	1.3346	0.416407	7.0363	2	1545400	717650	827700	95	540;3017	True;True	540;3018	858;4749

33.515	296	296;232;16	5.30E-75	1.1496	1.3346	0.416407	10.972	7	20625000	9462900	11162000	584	504;799;16	True;True;	504;799;16	808;1259;2
30.772	283	283;251;15	2.46E-72	1.0871	1.3335	0.415218	12.325	13	61071000	29313000	31758000	571	1228;2001	True;True;	1228;2001	1908;3130
52.645	480	480;222	3.46E-06	1.0379	1.3322	0.413811	4.2633	2	7302500	3675300	3627200	230	47;1289	True;True	47;1289	79;2021
61.054	573	573;517;44	0	1.0677	1.3253	0.406319	8.5243	65	672380000	3.2E+08	3.53E+08	870	29;216;258	True;True;	29;216;258	40;41;365;
35.619	322	322	1.27E-24	1.1381	1.3172	0.397474	2.8769	3	4703900	2247800	2456100	156	2179;2296	True;True;	2179;2296	3376;3573
20.694	189	189	2.80E-20	0.97949	1.3059	0.385044	8.3564	2	3951700	1957700	1994100	509	759;2275	True;True	759;2275	1200;3542
104.85	911	911;521;34	1.23E-190	1.0666	1.3015	0.380175	5.7186	22	58642000	28238000	30403000	229	126;177;42	True;True;	126;177;42	212;286;71
410.2	3925	3925	0.017482	1.0134	1.3011	0.379732	5.4317	2	12790000	6230900	6558700	850	1591	TRUE	1591	2490;2491
23.264	219	219;219;20	5.12E-07	1.0462	1.2997	0.378179	7.965	2	2147800	1056200	1091600	34	3058;3191	True;True	3059;3192	4816;5044
32.866	298	298;158;72	4.74E-30	1.0577	1.2955	0.373509	17.521	4	8001000	3531200	4469700	667	35;436;786	True;True;	35;436;786	53;54;722;
29.357	258	258;249;23	1.95E-10	1.0044	1.2947	0.372618	10.762	2	4081800	1910500	2171300	847	510;874;12	True;False;	510;874;12	815;1362;1
30.886	267	267;254;13	1.06E-35	1.0503	1.2865	0.363451	4.9628	4	5245200	2504700	2740500	455	1538;2582	True;True;	1538;2582	2414;2415
38.631	341	341;330;42	1.75E-17	1.0147	1.2753	0.350837	10.755	4	6267400	3184600	3082800	425	705;1573;1	True;True;	705;1573;1	1111;2469
11.367	103	103	2.75E-20	0.95646	1.2752	0.350724	11.806	7	18539000	9188800	9350300	801	419;537;15	True;True;	419;537;15	701;853;85
37.535	341	341;317;29	1.01E-05	1.012	1.2719	0.346985	20.502	2	1678700	847520	831170	713	2868;2984	True;True	2869;2985	4515;4700
38.388	333	333;327	5.65E-06	0.99069	1.2702	0.345056	26.025	2	4370900	2268600	2102300	336	615;2592	True;True	615;2592	989;4049
20.55	182	182;181;16	0.006307	1.021	1.2684	0.34301	6.2296	2	1186700	582820	603880	542	692;3398	True;True	692;3399	1082;5379
15.388	136	136;136;13	1.81E-06	0.96355	1.2601	0.333538	0.80499	2	12072000	4718700	7352800	535	2634;3408	True;True	2635;3409	4116;5397
32.996	298	298;297	2.10E-13	1.0268	1.2577	0.330788	11.22	4	5452800	2778000	2674700	821	740;1575;2	True;True;	740;1575;2	1167;1168
26.923	261	261;252;16	4.09E-41	1.0324	1.2563	0.329181	5.5013	5	12350000	5879700	6470700	278	492;603;10	True;True;	492;603;10	796;961;16
19.856	169	169	2.26E-08	1.0048	1.2483	0.319965	8.9312	2	2140000	1071400	1068600	464	818;828	True;True	818;828	1280;1295
42.123	390	390;318;31	1.23E-12	0.99847	1.2451	0.316262	6.9611	5	11439000	5851400	5587200	679	577;1881;2	True;True;	577;1881;2	924;925;29
73.68	679	679;632	5.79E-174	0.99505	1.2435	0.314407	14.291	26	121150000	58863000	62285000	133	277;405;18	True;True;	277;405;18	460;461;67
71.502	627	627;592;32	4.61E-30	1.0081	1.2416	0.3122	9.8481	7	12210000	6192000	6017800	322	61;701;119	True;True;	61;701;119	104;1098;1
20.546	178	178;178;16	6.33E-14	0.99894	1.241	0.311503	13.567	2	6119400	2894800	3224600	96	374;574	True;True	374;574	619;921
48.442	453	453	1.01E-40	0.96757	1.2349	0.304394	3.9033	3	7896000	3946500	3949600	728	302;2136;2	True;True;	302;2136;2	517;3322;4
23.277	213	213;86;74;	1.11E-48	1.0044	1.2348	0.304277	7.4388	6	16559000	8179600	8379700	129	1047;2066	True;True;	1047;2066	1661;3234
56.559	529	529;162;10	5.38E-146	0.96091	1.2337	0.302992	7.9652	33	169400000	84902000	84498000	722	130;133;92	True;True;	130;133;92	216;217;22
31.212	278	278;266;26	4.46E-21	1.0131	1.2328	0.301939	16.04	3	10467000	5048600	5418600	865	3365;3393	True;True;	3366;3394	5332;5374
71.122	661	661;631;63	3.70E-25	1.0006	1.2324	0.301471	16.201	5	5555800	2637700	2918000	431	1161;1874	True;True;	1161;1874	1810;2945
84.87	760	760;679	1.96E-12	1.0053	1.2251	0.2929	9.7804	4	3513900	1790600	1723400	349	1439;3192	True;True	1439;3193	2269;2270
51.146	464	464;378	3.22E-07	1.1682	1.2231	0.290542	15.434	7	159950000	71999000	87950000	883	571;572	True;True	571;572	912;913;91
77.028	685	685;351;30	8.64E-76	0.96273	1.2211	0.288181	31.505	19	67945000	35877000	32068000	543	802;2781;2	True;True;	802;2782;2	1263;4353
18.491	161	161;137;10	1.43E-36	0.97424	1.2103	0.275365	3.9745	4	11026000	5414200	5612000	632	119;1628;2	True;True;	119;1628;2	205;2564;4
32.816	302	302;285	1.72E-29	0.95616	1.2013	0.264596	8.0443	4	5445300	2714000	2731400	710	351;393;25	True;True;	351;393;25	593;643;40
26.049	236	236	0.000117	0.94159	1.1998	0.262794	16.69	2	3520500	1717300	1803200	860	1805	TRUE	1805	2851;2852
19.81	174	174;139	6.45E-05	0.9273	1.1997	0.262674	8.7502	2	3339900	1742000	1597900	72	162	TRUE	162	264;265
35.503	338	338;296;23	1.59E-95	0.99783	1.1994	0.262313	30.27	26	125580000	62741000	62837000	665	251;694;10	True;True;	251;694;10	421;422;42
101.27	866	866;865	0.000261	0.97477	1.1977	0.260267	17.99	2	1852300	980730	871580	477	1705;3001	True;True	1705;3002	2679;4726
20.313	180	180	2.67E-08	0.96603	1.1956	0.257735	8.9165	3	2384900	1269300	1115600	709	2215;2257	True;True;	2215;2257	3453;3515
59.75	553	553;531;21	3.31E-172	0.94103	1.1938	0.255561	8.7159	23	103820000	51956000	51862000	797	260;335;65	True;True;	260;335;65	433;434;56

70.289	627	627;196;24	0	1.0161	1.1934	0.255078	17.691	48	450760000	2.23E+08	2.28E+08	180	6;58;379;6	True;True;	6;58;379;6	6;99;625;6
81.673	737	737;732;51	6.02E-07	0.9464	1.1902	0.251204	0.25014	2	1136300	606710	529580	746	2454;3224	True;True	2454;3225	3816;5108
26.21	243	243;234	1.38E-05	0.9176	1.1871	0.247441	17.725	2	5963000	3175700	2787300	471	641	TRUE	641	1017;1018
19.608	180	180;134;30	5.39E-15	0.89043	1.1827	0.242084	19.471	6	17250000	9046200	8204100	594	66;67;477;	True;True;	66;67;477;	112;113;77
35.936	320	320;319	4.74E-86	0.9881	1.1811	0.240131	3.1194	16	57017000	28284000	28732000	741	508;509;91	True;True;	508;509;91	813;814;14
28.908	256	256;195;10	5.63E-09	0.93654	1.1768	0.234869	30.056	4	4557800	2290500	2267300	446	1658;3347	True;True;	1658;3348	2613;5301
43.66	395	395;299	4.60E-15	0.91094	1.1747	0.232292	1.2096	2	6414200	3192600	3221600	171	976;3373	True;True	976;3374	1539;5341
79.685	736	736;761	1.05E-30	1.0138	1.1733	0.230572	9.6043	5	5086800	2456000	2630800	313	370;1319;3	True;True;	370;1319;3	615;2060;2
72.421	655	655	2.49E-122	0.95031	1.1705	0.227125	10.196	26	75854000	38590000	37264000	67	735;1394;1	True;False;	735;1394;1	1161;1162
29.804	272	272;204;20	3.96E-113	0.95901	1.167	0.222805	7.7847	19	121320000	60538000	60785000	268	9;15;518;6	True;True;	9;15;518;6	9;10;11;12
52.164	466	466;308	1.98E-35	0.90485	1.1616	0.216113	13.505	5	9482400	4978200	4504300	208	625;1925;2	True;True;	625;1925;2	1000;3036
96.771	873	873;868	6.69E-34	0.9444	1.1604	0.214622	53.58	4	5530500	2519300	3011100	654	751;1821;2	True;True;	751;1821;2	1190;2873
46.836	408	408;361;18	1.12E-23	0.90791	1.1599	0.214	0.57114	2	6142800	3203600	2939100	151	1172;1385	True;True	1172;1385	1827;2180
21.612	188	188;179;16	2.02E-05	0.86513	1.1534	0.205893	23.351	2	1865600	930090	935520	513	1026;3026	True;True	1026;3027	1626;4762
30.354	276	276;276;27	8.85E-11	0.91427	1.1477	0.198746	9.2143	3	4877300	2571800	2305500	33	293;944;29	True;True;	293;944;30	504;1482;4
29.126	254	254;249;23	7.36E-94	0.913	1.147	0.197865	5.3732	11	22359000	11426000	10933000	757	99;244;132	True;True;	99;244;132	163;164;16
24.722	222	222;222;16	8.51E-24	0.92323	1.1469	0.19774	8.583	2	2568500	1237600	1330900	347	163;1030	True;True	163;1030	266;1631
68.741	631	631;623;54	5.94E-102	0.96022	1.1449	0.195222	9.7753	19	67968000	34331000	33638000	848	409;1269;1	True;True;	409;1269;1	689;1985;2
27.692	256	256;238	2.58E-40	0.92145	1.1447	0.19497	15.078	8	32151000	16616000	15535000	378	93;520;521	True;True;	93;520;521	156;827;82
273.42	2511	2511	1.33E-68	0.90188	1.1439	0.193961	10.658	13	20552000	10795000	9757600	413	120;198;28	True;True;	120;198;28	206;334;46
61.397	558	558;558	1.15E-07	0.89949	1.1428	0.192573	5.2674	3	4441800	2407200	2034600	263	2127;2677	True;True;	2127;2678	3310;4198
144.5	1262	1262;1055	1.22E-07	0.88175	1.1413	0.190678	6.5458	3	1192700	628940	563750	849	920;2093;3	True;True;	920;2093;3	1448;1449
94.33	840	840;148	2.77E-59	0.91601	1.139	0.187768	5.4488	8	20325000	10268000	10058000	62	94;109;670	True;True;	94;109;670	157;189;10
48.141	417	417;214	2.37E-23	0.91264	1.1389	0.187641	2.5172	3	9698100	4913500	4784600	318	785;987	True;True	785;987	1237;1552
42.403	376	376	1.64E-23	1.1872	1.1369	0.185105	8.0036	5	14796000	6503400	8292700	476	280;1256;1	True;True;	280;1256;1	464;465;19
26.477	239	239;232;22	1.65E-20	0.90456	1.1364	0.184471	2.2492	5	14106000	7370300	6735600	559	271;347;19	True;True;	271;347;19	453;587;30
87.819	805	805;780;49	1.57E-62	0.90921	1.1361	0.18409	3.8139	9	14272000	7585600	6686000	280	462;474;56	True;True;	462;474;56	756;774;89
12.855	108	108;129	2.47E-13	0.87217	1.1347	0.182311	5.8312	5	9392900	4835000	4557900	580	1426;1703	True;True;	1426;1703	2248;2677
16.893	149	149;148;14	6.56E-06	0.85449	1.1339	0.181293	14.724	2	7887900	4039800	3848200	416	758;2611	True;True	758;2611	1199;4073
134.46	1176	1176;1130	2.76E-16	0.90539	1.1329	0.180021	4.503	5	2331600	1223000	1108700	512	842;871;27	True;True;	842;871;27	1312;1359
18.157	161	161	2.11E-06	0.849	1.1319	0.178747	23.039	3	4136100	2044100	2091900	358	2750;2860	True;True;	2751;2861	4300;4506
44.503	416	416;386	5.44E-05	0.93391	1.1296	0.175812	1.2649	2	3491400	1765500	1725900	275	2798;3186	True;True	2799;3187	4386;5035
109.29	992	992;968	4.84E-30	0.93635	1.1291	0.175173	6.7194	6	9977700	5052000	4925700	426	337;362;11	True;True;	337;362;11	562;607;17
48.729	453	453;367;27	2.52E-42	0.87694	1.1281	0.173895	10.658	6	14476000	7473800	7002700	794	164;292;11	True;True;	164;292;11	267;268;50
109.96	962	962	1.42E-10	0.91809	1.128	0.173767	4.5391	2	2100900	1092100	1008800	731	453;1661	True;True	453;1661	745;2616
34.063	313	313;291	1.94E-13	0.892	1.1211	0.164915	26.167	4	3323100	1785800	1537300	237	137;140;28	True;True;	137;140;28	227;232;44
33.296	299	299;261	1.75E-109	0.94427	1.121	0.164786	10.923	18	100010000	49620000	50387000	420	278;283;51	True;True;	278;283;51	462;468;82
56.782	505	505;461;14	6.06E-34	0.88725	1.1196	0.162983	8.5672	6	15847000	8318100	7528600	384	756;1059;1	True;True;	756;1059;1	1197;1676
119.52	1038	1038	4.48E-35	0.89906	1.1195	0.162855	3.4011	5	4162000	2203600	1958300	127	80;144;809	True;True;	80;144;809	141;237;23
26.182	230	230;251	2.39E-07	0.90497	1.1189	0.162081	10.441	2	1857500	1027400	830090	192	3294;3378	True;True	3295;3379	5208;5349
92.468	803	803;553;16	5.67E-82	0.90536	1.1176	0.160404	6.484	13	43741000	22676000	21065000	419	478;624;74	True;True;	478;624;74	779;999;11

75.378	660	660;588	3.78E-14	0.88639	1.116	0.158337	22.629	3	5513600	2710900	2802700	89	1551;1724	True;True;	1551;1724	2430;2710
97.169	876	876;660	2.79E-68	0.89187	1.1155	0.157691	6.5436	15	34303000	18146000	16157000	49	30;573;10(	True;True;	30;573;10(	42;43;919;
33.371	309	309;294;29	6.60E-36	0.92416	1.1151	0.157173	8.6215	11	36179000	18810000	17369000	368	1050;2002	True;True;	1050;2002	1664;3132
68.996	647	647;542	8.31E-15	0.88565	1.115	0.157044	8.5195	5	16371000	8636200	7735300	330	467;1083;1	True;True;	467;1083;1	762;1716;1
39.591	366	366;331;28	5.40E-15	0.88323	1.1146	0.156526	3.3083	4	7611400	4004800	3606600	461	264;1287;2	True;True;	264;1287;2	445;2019;3
28.723	249	249;250	1.35E-39	0.9074	1.1132	0.154713	5.5697	10	34827000	17962000	16865000	824	265;266;13	True;True;	265;266;13	446;447;2(
57.136	501	501;182;17	7.48E-12	0.87763	1.1108	0.151599	17.648	2	2459100	1391500	1067600	577	41;798;95(	True;True;	41;798;95(	65;1258;14
50.464	456	456;353	5.68E-13	0.87972	1.1102	0.15082	6.188	2	1509200	784920	724240	787	1473;2757	True;True	1473;2758	2311;4317
71.496	625	625;597;42	7.30E-13	0.96122	1.11	0.15056	3.7369	3	8661500	4589200	4072300	242	1787;3226	True;True;	1787;3227	2819;5110
34.93	307	307	1.55E-11	0.88591	1.1089	0.149129	7.9502	3	7969200	4183700	3785500	763	319;2075	True;True	319;2075	539;3243;3
32.922	286	286;276;17	1.75E-48	0.87665	1.1063	0.145743	15.606	7	32970000	17370000	15600000	107	601;642;96	True;True;	601;642;96	959;1019;1
170.6	1512	1512;988	8.52E-19	0.86357	1.1043	0.143132	9.4653	5	5174700	2716300	2458400	223	1139;1902	True;True;	1139;1902	1783;3001
14.395	127	127;73	1.03E-22	0.83155	1.1034	0.141956	8.4941	2	6650000	3651700	2998300	646	787;1092	True;True	787;1092	1241;1728
49.042	439	439;431;43	2.45E-19	0.87008	1.1013	0.139208	31.091	2	2282500	1205200	1077300	508	941;2168	True;True	941;2168	1479;3364
78.365	709	709;694;38	6.99E-12	0.89394	1.101	0.138814	4.4204	2	2401200	1231800	1169400	869	1905;3405	True;True	1905;3406	3004;5394
36.014	323	323;318;26	0.000162	0.87455	1.0992	0.136454	3.3747	2	1592200	780420	811790	38	2380;2856	True;True	2380;2857	3705;4502
19.653	177	177;152;85	6.70E-33	0.83112	1.0976	0.134352	0.69753	2	5629900	3082600	2547300	203	558;926;10(	False;False	558;926;10(	883;884;88
30.241	264	264	1.96E-19	0.88741	1.0972	0.133827	5.6422	4	5181000	2627000	2554000	394	2362;2570	True;True;	2362;2570	3681;4018
14.839	130	130;388;12	4.50E-08	0.81496	1.0972	0.133827	7.9631	4	9808100	5355600	4452500	643	876;1564;2	True;True;	876;1564;2	1368;2446
55.804	514	514;470;27	4.38E-32	0.87887	1.0968	0.1333	7.1189	8	14154000	7599600	6554300	668	486;637;65	True;True;	486;637;65	788;1013;1
83.829	727	727;429;24	1.80E-06	0.87177	1.0964	0.132774	7.4886	2	1280400	645580	634780	618	1003;1949	True;True;	1003;1949	1580;3062
12.349	109	109	3.25E-05	0.82525	1.0944	0.13014	6.6625	2	1710100	883920	826210	163	2529	TRUE	2529	3919;3920
28.302	247	247;207	2.29E-74	0.88395	1.093	0.128293	25.154	4	23126000	11977000	11148000	635	376;566;16	True;False;	376;566;16	621;894;89
25.206	217	217;176;16	1.05E-09	0.89764	1.0923	0.127369	14.257	7	7559600	3907900	3651700	329	303;796;93	True;True;	303;796;93	518;1255;1
26.409	236	236;234;23	3.24E-47	0.87115	1.0922	0.127237	13.802	22	96412000	50898000	45515000	846	933;1259;1	True;True;	933;1259;1	1462;1463
55.52	491	491;368;47	4.20E-08	0.87496	1.0919	0.126841	4.9594	2	2057600	1108100	949550	298	1185;3090	True;True	1185;3091	1847;4884
15.945	142	142	4.60E-05	0.82464	1.089	0.123004	4.3985	3	10866000	5805600	5059900	277	36;734;841	True;True;	36;734;841	55;1160;13
26.489	241	241;196	7.57E-18	0.86728	1.0887	0.122606	9.1479	3	5851000	3163700	2687300	381	112;591;10(	True;True;	112;591;10(	194;941;16
37.331	340	340;340;34	1.66E-10	0.88923	1.0878	0.121413	7.149	3	5826100	3231400	2594700	66	1792;1882	True;True	1792;1882	2827;2954
103.28	919	919;478;26	1.94E-23	0.89262	1.0875	0.121015	4.3896	6	8223100	4222600	4000400	405	115;607;8(	True;True;	115;607;8(	198;966;12
98.16	854	854;732;53	1.38E-206	0.85141	1.0855	0.11836	11.065	33	129330000	69264000	60068000	753	46;212;25(	False;True;	46;212;25(	74;75;76;7
1011	8797	8797;8797	2.08E-05	0.8454	1.0853	0.118094	21.412	2	15615000	7894300	7720900	655	2382;3098	True;True	2382;3099	3707;4896
27.399	246	246;227;27	1.20E-25	0.86293	1.0841	0.116498	6.0618	5	15412000	8283000	7129400	450	151;1448;1	True;True;	151;1448;1	248;2279;2
126.97	1140	1140;1009	0.005109	0.83715	1.0836	0.115832	25.026	2	781790	411180	370610	676	3212;3234	True;True	3213;3235	5078;5122
32.004	289	289;255;25	0.000416	0.91173	1.082	0.1137	10.026	2	1597000	812760	784210	497	143	TRUE	143	235;236
44.36	398	398;397;39	1.38E-19	1.1298	1.0819	0.113567	9.1394	3	7268800	3440800	3828100	816	873;902;32	True;True;	873;902;32	1361;1405
15.798	136	136;80;40	3.22E-06	0.8152	1.0817	0.1133	0.98785	2	5786300	3121900	2664500	606	3248;3417	True;True	3249;3418	5141;5410
35.924	324	324;322;37	8.20E-57	0.83773	1.0812	0.112633	1.243	3	15792000	8483300	7308600	474	997;2170;2	True;True;	997;2170;2	1573;3366
39.146	372	372;357	1.65E-80	0.84609	1.0806	0.111833	5.372	7	30279000	16851000	13428000	859	640;921;14	True;True;	640;921;14	1016;1450
58.024	531	531;486;48	3.69E-87	0.86568	1.0803	0.111432	7.1914	10	22945000	12217000	10728000	435	225;1084;1	True;True;	225;1084;1	383;384;17
71.027	643	643;367	3.01E-38	0.85076	1.0798	0.110764	6.1008	5	27433000	15010000	12423000	747	305;1397;1	False;False	305;1397;1	520;2198;2

27.566	241	241;200;18	1.15E-08	0.88719	1.0796	0.110497	8.2737	3	7499000	3934900	3564100	310	1165;1242	True;True;	1165;1242	1814;1937
13.459	114	114	4.03E-06	0.7916	1.0787	0.109294	7.6879	4	5529500	3086600	2442900	541	985;2616	True;True	985;2616	1549;1550
86.267	790	790;788;44	3.58E-07	0.86349	1.0776	0.107822	2.3201	3	7994500	4116400	3878200	545	2509;2526	True;True	2509;2526	3888;3889
12.784	115	115;115;96	8.19E-14	0.80761	1.0767	0.106616	0.98072	2	2756500	1491600	1264900	607	2046;2964	True;True	2046;2965	3188;4661
21.868	191	191;191;18	3.75E-14	0.85754	1.0765	0.106348	7.3399	3	4094700	2236600	1858100	386	128;1965;3	True;True;	128;1965;3	214;3083;5
21.995	192	192	9.83E-07	0.8578	1.0762	0.105946	6.7598	3	2273500	1226600	1046900	636	649;2054;3	True;True;	649;2054;3	1027;3202
32.642	292	292;267;15	7.55E-30	0.79406	1.0751	0.104471	8.0821	11	55483000	30498000	24986000	841	558;559;92	True;True;	558;559;92	883;884;88
35.744	325	325;324;30	1.20E-15	0.85879	1.075	0.104337	7.052	3	2494800	1315400	1179400	772	1399;2035	True;True;	1399;2035	2202;3175
122.34	1162	1162;1162	1.49E-08	0.82853	1.0724	0.100843	8.9422	2	1138400	641020	497400	809	797;1797	True;True	797;1797	1257;2832
49.83	445	445;397;37	1.68E-202	0.8391	1.0716	0.099766	64.26	7	76230000	38353000	37877000	132	236;348;72	True;True;	236;348;72	395;396;58
60.343	556	556;401	5.99E-48	0.8506	1.0709	0.098824	9.2322	6	21068000	11043000	10025000	662	866;2294;2	True;True;	866;2294;2	1350;3571
37.434	346	346;255	7.67E-09	0.85208	1.0705	0.098285	7.213	3	3765600	2075600	1690000	90	700;1992;3	True;True;	700;1992;3	1097;3121
136.37	1230	1230;1062	1.71E-18	0.82666	1.07	0.097611	60.612	5	3515300	1796300	1719000	506	233;691;15	True;True;	233;691;15	392;1081;2
18.431	158	158;161	7.07E-12	0.84185	1.0682	0.095182	11.761	6	6927000	3956200	2970800	382	389;602;61	True;True;	389;602;61	638;960;97
23.356	210	210;174;52	3.16E-176	0.8518	1.0676	0.094371	6.0018	14	107520000	56668000	50850000	623	86;87;221;	True;True;	86;87;221;	149;150;37
25.898	234	234;164;48	4.68E-24	0.86229	1.0656	0.091666	3.1488	7	12837000	6849200	5987300	620	1234;1660	True;True;	1234;1660	1915;1916
80.109	704	704;495	4.20E-10	0.88321	1.065	0.090853	12.197	2	3858200	2179800	1678500	456	281;743	True;True	281;743	466;1178
37.482	335	335;272;27	3.46E-25	0.85681	1.0646	0.090311	13.883	7	10446000	5414300	5031500	596	1609;1723	True;True;	1609;1723	2528;2709
39.233	359	359;350;34	0.001685	0.84908	1.0628	0.08787	10.848	3	4654500	2458900	2195600	81	438;3255	True;True	438;3256	727;5151;5
16.363	145	145;103;14	3.26E-09	0.8043	1.0622	0.087055	9.767	3	5815000	3196800	2618200	308	1832;1928	True;True;	1832;1928	2886;3040
12.774	114	114	5.37E-19	0.8043	1.0622	0.087055	10.03	3	5559500	2987400	2572100	388	1033;2375	True;True;	1033;2375	1634;3696
20.762	176	176;154;17	1.26E-08	0.86184	1.0595	0.083384	4.0449	3	2000800	1007700	993120	403	531;986;21	True;True;	531;986;21	844;1551;3
33.969	301	301;301;28	1.14E-06	0.84291	1.0594	0.083247	1.5163	2	2503400	1382300	1121000	742	581;2130	True;True	581;2130	929;3315
20.697	181	181;181;17	1.01E-22	0.86167	1.0593	0.083111	13.778	3	4293200	2169100	2124200	561	418;2181	True;True	418;2181	700;3378;3
35.079	333	333;284;22	6.68E-29	0.87729	1.059	0.082703	5.3484	5	9006400	4770100	4236300	184	300;1119;1	True;True;	300;1119;1	514;1761;2
17.222	151	151	2.06E-16	0.78116	1.0582	0.081612	6.4642	4	8387700	4757300	3630400	642	1125;1794	True;True;	1125;1794	1767;2829
60.977	534	534	2.62E-12	0.84736	1.0575	0.080658	7.9376	3	4393600	2357700	2035900	197	929;1508;1	True;True;	929;1508;1	1458;2370
41.389	360	360;316	0.000229	1.1074	1.0567	0.079566	11.479	2	2860000	1231000	1629000	71	1162;2277	True;True	1162;2277	1811;3544
36.748	324	324;286;22	6.75E-31	0.89863	1.0564	0.079156	11.296	4	4597900	2417000	2180900	721	366;398;55	True;True;	366;398;55	611;664;87
31.362	282	282;178	1.35E-28	0.79654	1.0556	0.078063	4.547	3	12806000	7042100	5763600	241	98;2989	True;True	98;2990	161;162;47
23.742	216	216;178	3.44E-41	0.8386	1.0555	0.077927	8.5006	12	22753000	12089000	10664000	856	440;485;57	True;True;	440;485;57	729;786;78
176.53	1553	1553;1503	0.022656	0.9119	1.0554	0.07779	8.68	2	5854900	3072100	2782800	246	3207	TRUE	3208	5070;5071
57.488	535	535;130	4.48E-111	0.83889	1.0548	0.076969	12.252	10	24158000	12661000	11497000	694	412;632;64	True;True;	412;632;64	693;1008;1
51.153	449	449;445;40	1.41E-74	0.81784	1.0537	0.075464	9.3964	12	79645000	43959000	35685000	465	501;718;98	True;True;	501;718;98	805;1136;1
36.501	325	325;125	4.56E-08	0.84138	1.0532	0.074779	5.7806	3	6952600	3801300	3151400	213	674;2335;2	True;True;	674;2335;2	1058;3634
11.665	115	115	1.62E-77	0.79084	1.0529	0.074368	2.5041	6	30595000	16958000	13636000	147	1423;1665	True;True;	1423;1665	2244;2245
34.577	310	310	1.97E-07	0.86122	1.0529	0.074368	10.294	2	6878100	3728700	3149300	374	332	TRUE	332	555;556
19.41	168	168;157;15	8.34E-05	0.84657	1.0517	0.072723	1.7979	2	3646100	1989600	1656600	733	2336;3018	True;True	2336;3019	3635;4750
35.853	316	316;467;36	8.62E-08	0.8366	1.0515	0.072449	1.3007	2	5456700	2987700	2469000	779	611;2597;2	True;True;	611;2597;2	971;4054;4
70.67	636	636;636;54	1.91E-11	0.83411	1.0501	0.070527	7.87	7	9965500	5373200	4592300	145	671;958;10	True;True;	671;958;10	1053;1500
22.836	201	201;249	2.09E-26	0.83633	1.0499	0.070252	8.2957	4	10485000	5656400	4828900	438	908;2169;3	True;True;	908;2169;3	1420;1421

57.924	539	539;514;49	2.40E-47	0.84032	1.0497	0.069977	12.364	10	41123000	21443000	19680000	719	79;202;372	True;True;	79;202;372	140;340;34
89.656	793	793;775;76	1.03E-25	0.83559	1.0486	0.068464	8.9845	7	6166100	3387900	2778200	411	150;316;62	True;True;	150;316;62	247;534;99
13.742	125	125;124;63	5.16E-15	0.76151	1.0481	0.067776	11.778	5	25566000	14188000	11378000	211	20;484;180	True;True;	20;484;180	23;24;785;
21.676	198	198;183;15	3.80E-05	0.85243	1.048	0.067639	1.2223	2	1486100	818730	667410	418	1982;2514	True;True	1982;2514	3107;3898
52.878	475	475;391;24	5.28E-21	0.82669	1.048	0.067639	8.646	8	22380000	12500000	9879300	539	680;2343;2	True;True;	680;2343;2	1065;1066
39.611	350	350;257;21	2.26E-13	0.84688	1.0471	0.066399	2.3603	2	3768900	1976900	1791900	172	2053;2934	True;True	2053;2935	3201;4607
20.825	184	184;184;18	4.48E-13	0.85172	1.0471	0.066399	18.279	3	3913700	2138200	1775500	250	1467;2078	True;True;	1467;2078	2303;3247
49.874	455	455	9.77E-29	0.80916	1.0469	0.066124	6.5047	9	55818000	30259000	25559000	417	57;498;698	True;True;	57;498;698	98;802;109
274.61	2364	2364;2168	5.20E-245	0.82244	1.0466	0.06571	4.5461	26	55400000	30222000	25179000	101	239;413;49	True;True;	239;413;49	406;407;69
47.534	423	423;160	3.58E-22	0.80534	1.045	0.063503	18.503	6	25680000	13942000	11738000	514	70;1455;20	True;True;	70;1455;20	117;2287;3
59.366	543	543;499;50	1.38E-66	0.84866	1.0448	0.063227	4.2934	11	27027000	14547000	12479000	292	320;1827;1	True;True;	320;1827;1	540;541;28
32.604	294	294;248	1.97E-12	0.83695	1.0445	0.062812	6.0298	2	4243600	2203400	2040300	243	635;2891	True;True	635;2892	1011;4550
28.993	261	261;53;53	9.77E-19	0.83	1.0428	0.060462	4.8054	4	7768400	4232100	3536300	375	445;806;10	True;True;	445;806;10	735;1267;1
14.865	140	140;140;12	5.73E-32	0.78952	1.0427	0.060324	1.2401	3	11159000	6265600	4893600	170	1164;1510	True;True;	1164;1510	1813;2372
53.139	483	483;429;28	4.38E-93	0.80917	1.0423	0.059771	7.9122	9	70272000	38373000	31899000	617	123;1087;1	True;True;	123;1087;1	209;1722;2
26.056	233	233;232	1.52E-05	0.88654	1.0422	0.059632	2.1407	2	1617800	912210	705560	516	1491;1801	True;True	1491;1801	2338;2841
91.706	796	796;363	2.85E-18	0.82592	1.0391	0.055335	5.4708	5	5967100	3213500	2753600	299	65;1451;14	True;True;	65;1451;14	111;2282;2
17.718	152	152;152;14	8.39E-29	0.7864	1.0385	0.054501	3.1935	9	32718000	18305000	14413000	221	103;1291;1	True;True;	103;1291;1	173;2023;2
33.777	303	303	2.70E-19	0.82888	1.0375	0.053111	1.7678	2	3739800	2027800	1712000	87	2685;2828	True;True	2686;2829	4206;4447
28.836	248	248;201;20	2.20E-16	0.81718	1.0375	0.053111	2.4291	4	19186000	10283000	8902900	768	861;862;92	True;True;	861;862;92	1335;1336
53.9	492	492;440	9.12E-70	0.80726	1.0374	0.052972	11.519	5	35258000	19195000	16063000	704	179;1046;1	True;True;	179;1046;1	288;1660;1
140.47	1264	1264;1264	3.90E-07	0.80141	1.0373	0.052833	19.414	3	1217300	654720	562590	39	229;1951;2	True;True;	229;1951;2	388;3064;4
16.368	148	148;141;13	0.002002	0.7817	1.0373	0.052833	3.2763	2	2763400	1565100	1198300	112	153;2295	True;True	153;2295	250;3572
22.949	205	205;112;10	3.11E-31	0.8348	1.0371	0.052555	2.6881	4	13682000	7297000	6384600	437	896;1903;2	True;True;	896;1903;2	1399;3002
48.275	419	419;353;34	7.54E-06	0.82837	1.0369	0.052277	2.3613	3	12791000	6939900	5850900	889	322;1376;3	True;True;	322;1376;3	543;2160;4
32.551	293	293	2.05E-24	0.8503	1.0347	0.049213	23.402	5	6938400	3606900	3331500	276	2014;3010	True;True;	2014;3011	3148;3149
17.259	148	148;159;13	3.69E-42	0.78289	1.0339	0.048097	7.9201	5	20007000	11068000	8939200	451	582;2300;2	True;True;	582;2300;2	930;3579;3
33.712	305	305;222;19	1.38E-16	0.8647	1.0326	0.046282	4.2406	2	2491500	1330400	1161100	648	911;3086	True;True	911;3087	1424;4880
56.166	519	519;488;35	4.55E-19	0.82738	1.0325	0.046142	14.019	4	8949500	4900600	4048900	788	1094;1134	True;True;	1094;1134	1730;1778
22.677	205	205;205;20	7.84E-13	0.8395	1.0321	0.045583	8.1975	5	15971000	8765100	7206200	104	665;1854;2	True;True;	665;1854;2	1045;1046
23.489	207	207;160;15	3.07E-64	0.83954	1.0321	0.045583	6.7185	6	18601000	10083000	8517600	258	318;541;62	True;True;	318;541;62	538;859;10
51.712	466	466;431;42	1.68E-25	0.80527	1.0317	0.045024	74.922	6	56553000	21120000	35433000	391	195;472;10	True;True;	195;472;10	331;772;16
110.42	971	971;945;76	5.43E-146	0.84576	1.0316	0.044884	4.7561	14	26893000	14261000	12631000	353	7;497;1390	True;True;	7;497;1390	7;801;2185
12.985	115	115;115;11	1.27E-10	0.77676	1.0307	0.043624	3.8557	2	5666800	3156400	2510400	770	475;2183	True;True	475;2183	775;3381
36.112	315	315	1.71E-23	0.82296	1.0301	0.042784	2.148	3	4424700	2363600	2061100	621	1466;2714	True;True;	1466;2715	2302;4244
26.411	241	241	7.67E-14	0.81902	1.029	0.041243	4.5556	3	10596000	5699100	4896800	669	1213;1734	True;True;	1213;1734	1885;2721
28.777	248	248;237;21	0.003909	0.83187	1.0286	0.040682	1.647	2	993200	534640	458570	430	648;3279	True;True	648;3280	1026;5181
50.14	462	462;462;46	1.04E-52	0.80803	1.0281	0.039981	12.687	42	471660000	2.58E+08	2.14E+08	766	697;838;13	True;True;	697;838;13	1088;1089
26.227	227	227	1.16E-14	0.80646	1.028	0.03984	7.9326	5	6814100	3915800	2898400	857	192;1731;1	True;True;	192;1731;1	328;2718;3
24.454	220	220;199;18	1.05E-96	0.83342	1.0265	0.037734	4.9023	8	21741000	11964000	9777100	832	426;427;45	True;True;	426;427;45	709;710;75
469.08	4128	4128;4097	2.18E-38	0.80535	1.0249	0.035483	10.367	9	7807400	4282600	3524700	688	21;980;176	True;True;	21;980;176	25;1543;27

20.252	178	178;177;17	8.42E-28	0.82453	1.0247	0.035202	0.36263	2	9338800	5059300	4279600	752	3096;3319	True;True	3097;3320	4894;5240
34.273	317	317;317;25	7.14E-58	0.82154	1.0246	0.035061	21.933	14	74796000	40510000	34286000	148	85;102;385	True;True;	85;102;385	146;147;14
112.42	998	998;978;97	5.30E-15	0.80681	1.0243	0.034638	28.491	4	2468300	1110300	1358100	493	555;859;25	True;True;	555;859;25	876;1333;4
18.829	175	175;126;12	1.70E-08	0.77193	1.0243	0.034638	6.761	2	8008300	4410800	3597500	282	918;2948	True;True	918;2949	1446;4641
46.937	416	416;396;27	1.75E-11	0.9421	1.0233	0.033229	15.116	4	5157800	2760500	2397300	568	1362;1471	True;True	1362;1471	2141;2142
45.376	399	399;394;30	2.73E-17	1.0714	1.0224	0.03196	0.35164	2	4546000	2207800	2338200	94	1226;1680	True;True	1226;1680	1906;2646
48.633	433	433;249;13	9.56E-12	0.801	1.0223	0.031819	5.1263	3	7534200	4125400	3408800	332	176;977;12	True;True;	176;977;12	285;1540;1
42.741	379	379	6.82E-06	1.1285	1.0223	0.031819	9.3358	2	1929400	943070	986340	428	949;2923	True;True	949;2924	1487;4592
20.9	183	183	3.72E-05	0.82263	1.022	0.031395	0.41469	2	1459500	759530	700010	350	473;1077	True;True	473;1077	773;1702
27.887	248	248;178;25	3.90E-63	0.82658	1.022	0.031395	8.7388	6	26939000	14533000	12405000	370	159;210;14	True;True;	159;210;14	258;352;22
39.837	361	361;332;33	9.77E-85	0.85739	1.0218	0.031113	11.08	28	227600000	1.2E+08	1.08E+08	586	489;548;54	True;True;	489;548;54	791;792;79
166.57	1382	1382	1.95E-33	0.79781	1.0214	0.030548	3.0439	9	12753000	7039800	5712800	444	249;931;16	True;True;	249;931;16	417;418;14
50.909	452	452;419;41	3.46E-117	0.79375	1.0205	0.029276	4.3434	11	57434000	32382000	25052000	188	309;490;55	True;True;	309;490;55	525;794;87
16.273	151	151	1.48E-15	0.76544	1.0205	0.029276	2.0686	2	11504000	6339200	5165000	406	1326;2844	True;True	1326;2845	2071;4484
37.54	337	337	4.32E-38	0.8196	1.0204	0.029135	16.667	11	77055000	42026000	35029000	863	172;1757;1	True;True;	172;1757;1	279;280;27
55.992	504	504;483;44	4.43E-89	0.80471	1.0201	0.028711	7.0266	23	159140000	87316000	71820000	56	16;91;247;	True;True;	16;91;247;	19;154;415
33.269	311	311	0.001713	0.83767	1.0193	0.027579	1.8411	2	2588000	1399800	1188200	408	892;1547	True;True	892;1547	1395;2425
36.638	334	334;232;13	1.84E-71	0.86276	1.0193	0.027579	10.983	22	179160000	93723000	85436000	609	906;1128;1	True;True;	906;1128;1	1412;1413
42.2	385	385;269;20	3.65E-05	0.79253	1.0192	0.027437	1.5384	2	4228800	2235300	1993500	312	1167;2484	True;True	1167;2484	1816;3856
52.739	488	488;466;43	4.47E-12	0.79143	1.0164	0.023468	0.9469	4	15166000	8548600	6617500	55	669;1000;1	True;True;	669;1000;1	1051;1576
22.367	198	198;198;12	2.97E-14	0.82674	1.0164	0.023468	0.42861	2	8238100	4399500	3838600	254	704;2042	True;True	704;2042	1110;3183
23.466	196	196;196	1.85E-27	0.83496	1.016	0.0229	7.7987	2	4251200	2439600	1811600	389	1817;3260	True;True	1817;3261	2869;5157
19.148	169	169;163;13	2.99E-09	0.79533	1.0145	0.020769	4.2046	4	4002300	2300800	1701600	550	1223;2398	True;True;	1223;2398	1902;1903
101.11	900	900;635;99	1.97E-41	0.84348	1.0144	0.020627	106.67	6	9419100	5168900	4250100	138	1066;1536	True;True;	1066;1536	1687;2412
51.721	469	469;458;45	1.13E-12	0.8114	1.014	0.020058	3.6937	3	9245600	4884700	4361000	652	514;1579;2	True;True;	514;1579;2	819;2476;3
96.864	858	858;814;86	1.10E-119	0.81941	1.0137	0.019631	67.746	16	34129000	18318000	15810000	598	90;108;479	True;True;	90;108;479	153;188;78
111.02	1037	1037;1023	0.000258	0.92875	1.0132	0.018919	21.694	2	4007100	2097200	1909900	113	1855	TRUE	1855	2921;2922
47.475	430	430;387;18	2.83E-91	1.0686	1.0131	0.018777	20.841	11	36602000	17374000	19229000	286	290;403;98	True;True;	290;403;98	501;676;15
24.831	217	217;217;13	1.38E-12	0.77768	1.013	0.018634	6.3451	3	6149000	3425400	2723700	776	575;1621	True;True	575;1621	922;2551;2
95.337	858	858;566;15	7.36E-190	0.81	1.0122	0.017494	45.693	56	172540000	94055000	78485000	554	114;209;28	True;True;	114;209;28	197;349;35
18.254	153	153;145;14	6.86E-07	0.80626	1.0121	0.017352	4.028	3	3558500	1914200	1644300	123	425;928;34	True;True;	425;928;34	708;1457;5
45.626	406	406;398;34	1.14E-22	0.79383	1.0114	0.016354	6.5236	2	3309500	1986500	1323000	365	1328;2831	True;True	1328;2832	2073;4450
52.22	445	445;172	4.10E-21	0.78444	1.0088	0.01264	14.552	9	41136000	22192000	18944000	216	2109;2117	True;True;	2109;2117	3283;3293
69.147	614	614;544;73	2.15E-14	0.85158	1.0084	0.012068	5.0813	4	10413000	5650800	4762400	274	263;1868;2	True;True;	263;1868;2	443;444;29
157.9	1394	1394;531;5	2.68E-109	0.80959	1.0083	0.011925	9.4276	29	25000000	13852000	11148000	868	129;402;40	True;True;	129;402;40	215;675;68
59.62	548	548;547;32	5.48E-105	0.80427	1.007	0.010064	5.8073	21	72471000	39585000	32886000	718	132;257;33	True;True;	132;257;33	220;430;55
54.889	484	484;745;49	6.86E-07	0.79087	1.0068	0.009777	30.649	5	6589100	3538700	3050400	895	2137;2580	True;True;	2137;2580	3323;3324
16.561	148	148	0.001025	0.77794	1.0064	0.009204	2.8174	2	4351700	2426800	1924900	806	2732	TRUE	2733	4271;4272
44.614	417	417;327;28	3.00E-192	0.7876	1.006	0.00863	16.418	20	219360000	1.19E+08	1E+08	531	37;131;188	True;True;	37;131;188	56;57;58;5
22.127	194	194;194;17	7.81E-13	0.81752	1.0051	0.007339	9.9603	5	9197400	4953900	4243600	222	147;598;74	True;True;	147;598;74	241;242;95
29.062	258	258;204	8.02E-11	0.803	1.0051	0.007339	6.0021	2	1838400	941480	896940	661	1533;1706	True;True	1533;1706	2408;2680

17.818	165	165;132;11	3.00E-65	0.80741	1.0049	0.007052	4.4705	7	31971000	17419000	14553000	380	390;711;12	True;True;	390;711;12	639;1127;1
34.324	312	312;98	2.40E-06	0.81249	1.0046	0.006621	5.7669	2	2069800	1134700	935080	130	1202;1520	True;True	1202;1520	1868;2392
20.777	184	184	4.86E-38	0.77882	1.0045	0.006478	7.0444	6	11654000	6428500	5225100	638	439;1056;1	True;True;	439;1056;1	728;1672;1
26.21	228	228;201;20	5.15E-16	0.79409	1.0035	0.005041	3.7853	5	17903000	10173000	7729100	761	68;1512;15	True;True;	68;1512;15	114;2376;2
57.116	508	508;452;22	1.16E-42	0.79269	1.0033	0.004753	8.9136	4	10898000	6083000	4814600	183	460;621;29	True;True;	460;621;29	754;996;45
37.551	334	334;323;30	4.26E-20	0.88744	1.0019	0.002739	15.686	5	7032300	3786400	3246000	53	341;1721;3	True;True;	341;1721;3	580;2705;2
41.331	369	369;359;14	3.43E-53	0.77612	1.0016	0.002306	8.998	6	100930000	55471000	45463000	478	138;139;16	True;True;	138;139;16	228;229;23
32.575	294	294;265;25	6.44E-21	0.80098	1.0016	0.002306	14.001	7	34966000	18395000	16571000	637	1153;2125	True;True;	1153;2125	1800;1801
29.999	268	268;238	1.72E-21	0.73394	1.0015	0.002162	5.8522	5	11916000	6658600	5257300	273	883;940;17	True;True;	883;940;17	1377;1478
22.11	199	199;171;97	1.04E-30	0.78449	1.0014	0.002018	7.8173	13	81840000	44983000	36857000	40	40;306;476	True;True;	40;306;476	63;64;521;
45.151	406	406;394;37	5.96E-38	0.77781	1.0009	0.001298	3.6822	7	28969000	16284000	12685000	699	82;214;676	True;True;	82;214;676	143;363;10
26.922	241	241;162	3.90E-47	0.80786	1.0008	0.001154	9.7988	6	20921000	11542000	9378300	187	1064;1217	True;True;	1064;1217	1685;1890
70.897	646	646;494;49	1.19E-222	0.81639	0.99982	-0.00026	34.918	71	362040000	1.97E+08	1.66E+08	78	288;406;69	True;True;	288;406;69	495;496;49
16.445	146	146;146;15	5.61E-19	0.74162	0.9991	-0.0013	6.7979	8	38222000	21580000	16642000	644	243;709;85	True;True;	243;709;85	411;1124;1
189.25	1657	1657;1631	2.45E-104	0.78141	0.99877	-0.00178	9.186	17	15737000	8726000	7011100	155	315;788;12	True;True;	315;788;12	533;1242;1
22.026	214	214;170;16	2.03E-16	0.75569	0.99799	-0.0029	2.0259	4	8082800	4480100	3602700	377	1205;1816	True;True;	1205;1816	1871;2868
29.815	261	261;239;21	1.08E-26	0.84888	0.99794	-0.00298	4.5418	4	7812900	3987800	3825100	658	666;2349;2	True;True;	666;2349;2	1047;3668
23.787	220	220;215;21	1.76E-09	0.80651	0.9972	-0.00405	3.22	2	4940500	2557500	2383000	499	2032;2960	True;True	2032;2961	3172;4657
16.005	142	142;119;61	6.57E-20	0.74734	0.9964	-0.0052	10.061	5	26466000	14845000	11621000	209	1785;2851	True;True;	1785;2852	2816;2817
284.54	2472	2472;2452	0	0.77975	0.99519	-0.00696	74.877	49	86345000	49167000	37178000	878	17;18;53;2	True;True;	17;18;53;2	20;21;88;3
72.777	646	646;581;12	4.96E-15	0.83217	0.99488	-0.00741	15.953	4	5357000	2889700	2467300	397	234;326;13	True;True;	234;326;13	393;547;20
35.594	309	309;309;30	2.89E-24	0.83725	0.99438	-0.00813	6.0321	3	5188000	2719200	2468800	140	2593;3411	True;True	2593;3412	4050;5403
17.84	164	164;163;13	6.51E-07	0.8	0.99386	-0.00889	2.654	2	2418200	1338500	1079700	755	904;968	True;True	904;968	1407;1528
24.74	215	215	1.30E-24	0.80468	0.99338	-0.00958	3.7664	3	2480300	1425100	1055200	118	1035;1460	True;True;	1035;1460	1642;2294
56.149	487	487;437;43	4.37E-82	0.78399	0.99289	-0.01029	16.284	19	157790000	86002000	71788000	41	3;201;343;	True;True;	3;201;343;	3;337;338;
24.65	227	227;286;28	1.54E-47	0.76224	0.99283	-0.01038	7.95	9	34113000	19496000	14617000	774	180;428;76	True;True;	180;428;76	289;290;71
60.533	545	545;544;50	1.42E-57	0.82106	0.99223	-0.01125	15.096	15	63585000	34153000	29432000	663	175;248;33	True;True;	175;248;33	284;416;55
30.791	286	286;249;21	5.75E-134	0.78453	0.99069	-0.01349	8.8757	18	109020000	59702000	49317000	807	422;731;88	True;True;	422;731;88	705;1157;1
83.263	724	724;597;16	3.03E-274	0.78745	0.99058	-0.01365	10.157	108	527360000	2.91E+08	2.37E+08	782	46;211;657	True;True;	46;211;657	74;75;76;7
100.2	908	908;778;74	1.33E-06	0.79583	0.98877	-0.01629	1.0658	3	5470400	3133600	2336800	206	350;1898	True;True	350;1898	591;592;29
15.054	140	140;140	2.89E-33	0.73842	0.98738	-0.01832	4.1963	4	54832000	30480000	24351000	576	562;564;26	True;True;	562;564;26	890;892;41
46.153	406	406;146	4.38E-46	0.77547	0.9872	-0.01859	8.5173	11	70396000	39204000	31192000	392	323;663;10	True;True;	323;663;10	544;1043;1
31.629	280	280	6.92E-09	0.81119	0.9871	-0.01873	7.2011	3	4080800	2231900	1848800	683	532;1940;2	True;True;	532;1940;2	845;3053;3
27.745	245	245;170;98	4.61E-148	0.7933	0.98635	-0.01983	7.3924	9	45299000	24875000	20424000	325	464;566;77	True;False;	464;566;77	758;894;89
41.924	397	397;397	3.71E-52	1.0371	0.98611	-0.02018	5.0658	3	10446000	4868400	5577600	46	442;816;28	True;True;	442;816;28	731;1278;4
29.174	255	255;193;26	7.35E-79	0.79031	0.98605	-0.02027	6.7466	14	81055000	44241000	36814000	37	10;26;566;	True;True;	10;26;566;	13;33;894;
64.324	569	569;558;53	9.39E-86	0.78984	0.9857	-0.02078	6.3854	8	22968000	12978000	9989900	432	344;844;12	True;True;	344;844;12	584;1314;1
81.307	719	719;543;38	4.07E-47	0.76725	0.98525	-0.02144	6.7035	8	11409000	6504700	4904300	707	116;213;11	True;True;	116;213;11	199;362;18
14.515	132	132;133	2.11E-06	0.74589	0.98504	-0.02175	10.64	3	9511300	5497300	4014100	235	593;1752;2	True;True;	593;1752;2	944;2755;4
30.375	275	275;224;21	4.44E-05	0.78447	0.98479	-0.02211	17.138	2	1784100	987860	796220	236	596;924	True;True	596;924	948;1453
176.23	1606	1606;1600	2.85E-14	0.77045	0.98477	-0.02214	14.013	4	3561000	1984400	1576600	760	618;645;66	True;True;	618;645;66	993;1022;1

69.284	611	611;537;5(	3.44E-12	0.78215	0.98473	-0.0222	4.4721	2	4650500	2589000	2061500	603	2077;3283	True;True	2077;3284	3246;5185
49.122	422	422	2.10E-34	0.8044	0.98435	-0.02276	3.1412	3	7062200	3995500	3066800	804	46;1272;15	False;True;	46;1272;15	74;75;76;7
83.139	739	739;685	2.56E-27	0.77746	0.98393	-0.02337	7.3819	6	8082700	4442100	3640600	867	1578;1833	True;True;	1578;1833	2475;2887
20.457	177	177;172;17	2.22E-12	0.78377	0.98392	-0.02339	1.214	3	3805900	2173400	1632500	484	965;1142;1	True;True;	965;1142;1	1523;1787
14.787	128	128;95;80	4.33E-14	0.74138	0.98376	-0.02362	12.534	2	14264000	8056000	6207600	605	121;1543	True;True	121;1543	207;2420
30.239	269	269;263;26	2.96E-33	0.78265	0.98326	-0.02436	4.6657	5	17942000	9805800	8136500	264	814;975;2(	True;True;	814;975;2(	1275;1538
28.068	244	244;244	8.85E-44	0.80013	0.98284	-0.02497	7.4865	7	11657000	6293100	5363800	119	127;688;14	True;True;	127;688;14	213;1078;2
72.932	645	645;166	1.13E-14	0.76534	0.98281	-0.02502	10.674	3	3974600	2185400	1789200	162	877;1306;2	True;True;	877;1306;2	1369;2043
28.082	246	246;244;1(	1.82E-71	0.77543	0.98174	-0.02659	13.556	6	23927000	13336000	10591000	572	357;566;77	True;False;	357;566;77	601;894;89
54.231	471	471;382;24	2.10E-17	0.76362	0.98027	-0.02875	12.575	4	6832700	3751500	3081200	723	105;361;86	True;False;	105;361;86	175;605;6(
21.916	194	194;158;15	2.86E-06	0.79726	0.98015	-0.02893	6.5315	2	8028100	4328900	3699200	326	1651;2088	True;True	1651;2088	2601;3261
24.893	215	215;216;16	2.51E-29	0.76701	0.97904	-0.03056	7.7684	18	43570000	24957000	18613000	789	913;1040;1	True;True;	913;1040;1	1426;1651
16.06	145	145	2.00E-25	0.73503	0.9781	-0.03195	4.0399	7	31032000	17536000	13496000	556	166;599;73	True;True;	166;599;73	272;957;11
47.766	426	426;464;37	4.38E-254	0.76176	0.97807	-0.03199	8.7768	50	565280000	3.13E+08	2.52E+08	855	149;238;82	True;True;	149;238;82	244;245;24
69.412	586	586;586;14	1.63E-31	0.78608	0.97732	-0.0331	7.4692	13	29426000	16223000	13203000	879	227;254;76	True;True;	227;254;76	386;426;42
71.407	647	647;646;28	8.66E-77	0.80482	0.97666	-0.03407	8.378	13	55870000	30666000	25204000	359	993;1222;1	True;True;	993;1222;1	1566;1900
94.68	925	925;219;21	8.24E-73	0.79833	0.97605	-0.03497	4.4755	8	45569000	24971000	20598000	363	469;1325;2	True;True;	469;1325;2	764;2068;2
102.35	898	898;890;84	2.06E-05	0.80899	0.97554	-0.03573	1.5889	2	1797200	994250	802990	371	2386;3409	True;True	2386;3410	3723;5399
47.716	432	432;404	1.66E-45	0.75909	0.9752	-0.03623	24.142	14	113780000	59613000	54165000	201	117;452;8(	True;True;	117;452;8(	200;744;12
19.448	165	165;163;16	1.92E-16	0.75867	0.97365	-0.03852	20.982	4	6258700	3619400	2639300	249	600;1045;2	True;True;	600;1045;2	958;1659;3
31.462	282	282;253;23	4.68E-18	0.81529	0.97357	-0.03864	8.5226	4	6174400	3337800	2836600	775	95;371;868	True;True;	95;371;868	158;616;13
123.8	1134	1134;1066	6.36E-06	0.76667	0.97334	-0.03898	4.5119	2	585590	325710	259870	666	766;1480;2	True;True;	766;1480;2	1208;2319
269.76	2541	2541;2542	3.07E-146	0.76606	0.97328	-0.03907	8.5878	20	22767000	12775000	9991800	698	194;230;32	True;True;	194;230;32	330;389;55
82.593	744	744;739;56	1.34E-18	0.77723	0.97237	-0.04042	1.551	4	3646900	2093400	1553500	114	72;1828;21	True;True;	72;1828;21	120;2882;3
39.681	363	363;336;3(	5.08E-15	0.77681	0.97235	-0.04045	15.427	3	3557900	1968500	1589400	270	1502;3064	True;True;	1502;3065	2356;4828
24.033	209	209	1.62E-16	0.77358	0.97188	-0.04115	2.6184	3	8886800	4793200	4093600	604	1417;2123	True;False;	1417;2123	2235;2236
51.294	474	474;351;17	1.78E-07	0.75315	0.97177	-0.04131	5.7131	3	8083300	4718300	3365000	355	1623;2273	True;True;	1623;2273	2554;3540
69.993	666	666;655;65	5.46E-05	0.75393	0.97169	-0.04143	0.22626	2	1065000	610420	454600	749	364;365;14	False;False	364;365;14	609;610;23
17.138	152	152;144;15	2.67E-14	0.73526	0.97101	-0.04244	3.2859	4	15979000	9117100	6862400	83	1305;1576	True;True;	1305;1576	2042;2473
47.168	434	434;341	3.25E-252	0.75859	0.97051	-0.04319	13.85	45	647200000	3.63E+08	2.84E+08	811	33;415;416	True;True;	33;415;416	46;47;48;4
51.156	463	463;255	1.56E-23	0.75493	0.96975	-0.04432	5.738	4	11124000	6491000	4633200	152	345;2713;2	True;True;	345;2714;2	585;4243;4
83.677	758	758;747;72	7.53E-19	0.77074	0.9693	-0.04498	8.0437	4	5940000	3235600	2704400	166	733;1967;2	True;True;	733;1967;2	1159;3087
24.763	225	225;123;68	4.10E-35	0.7723	0.96915	-0.04521	6.3167	3	23228000	12896000	10332000	540	2530;2588	True;True	2530;2588	3921;4040
50.227	456	456;386;26	2.19E-41	0.75916	0.96913	-0.04524	9.087	13	32223000	18081000	14141000	324	189;346;11	True;True;	189;346;11	321;322;32
28.433	255	255;248	2.12E-10	0.79623	0.9689	-0.04558	13.665	3	8627200	4884200	3743000	533	336;2578;3	True;True;	336;2578;3	561;4028;4
34.778	303	303;297;24	1.60E-40	0.83004	0.96872	-0.04585	29.554	8	22781000	12022000	10759000	412	200;1349;1	True;True;	200;1349;1	336;2114;2
51.855	475	475;474;43	1.01E-29	0.77614	0.9686	-0.04603	5.8502	2	4698900	2685300	2013700	139	1964;2998	True;True	1964;2999	3082;4722
29.483	261	261;235;23	8.60E-12	0.77213	0.96834	-0.04641	6.8878	6	17377000	9749600	7627300	703	829;1822;2	True;True;	829;1822;2	1296;2874
18.502	166	166;112;16	1.40E-112	0.76685	0.96788	-0.0471	4.4277	7	63621000	35521000	28100000	202	342;715;12	True;True;	342;715;12	581;582;11
89.321	806	806;160;11	6.03E-139	0.78909	0.96626	-0.04952	16.363	27	59460000	31396000	28064000	354	136;146;58	True;True;	136;146;58	226;240;93
24.279	211	211;211;1(	6.09E-23	0.79376	0.9659	-0.05005	2.456	3	8683400	4961000	3722500	767	2635;2772	True;True;	2636;2773	4117;4343

24.205	208	208;188	2.49E-37	0.77533	0.96496	-0.05146	2.949	4	7938200	4375800	3562500	574	1384;1515	True;True;	1384;1515	2178;2179
86.86	756	756;723;6(	2.46E-09	0.7666	0.96409	-0.05276	22.311	2	1667400	906700	760650	739	1060;1574	True;True;	1060;1574	1677;2470
35.554	318	318;150	2.95E-11	0.75273	0.96381	-0.05318	19.487	5	10033000	6095900	3937100	560	696;1011;2	True;True;	696;1011;2	1087;1602
21.634	188	188;137	3.56E-24	0.77507	0.96288	-0.05457	5.7479	2	5992300	3366700	2625600	555	1449;2697	True;True	1449;2698	2280;4225
59.67	541	541;486;28	3.40E-40	0.81476	0.9628	-0.05469	8.8771	7	22765000	12413000	10352000	181	358;585;95	True;True;	358;585;95	602;933;14
33.313	300	300;295;26	1.32E-65	0.77851	0.96274	-0.05478	15.125	14	108680000	59699000	48986000	778	160;851;96	True;True;	160;851;96	259;260;26
59.632	557	557;550;53	1.57E-36	0.75061	0.96208	-0.05577	9.9693	4	6226500	3527400	2699100	546	1295;2219	True;True;	1295;2219	2027;2028
18.658	163	163;168;16	3.43E-06	0.78239	0.96187	-0.05609	6.4769	3	4405900	2535500	1870400	714	2149;2702	True;True	2149;2703	3339;4230
292.74	2671	2671;140;9	1.09E-111	0.75448	0.96173	-0.0563	7.4625	25	28564000	16286000	12278000	43	19;27;148;	True;True;	19;27;148;	22;34;243;
27.349	246	246;232;20	1.37E-12	0.77263	0.96022	-0.05856	2.578	2	3538500	1894200	1644200	492	275	TRUE	275	457;458
113.08	1014	1014;250	1.55E-17	0.74746	0.95919	-0.06011	5.0405	3	2458100	1369800	1088300	799	74;2795;32	True;True;	74;2796;32	123;4383;5
25.035	224	224;101	1.36E-38	0.77841	0.95875	-0.06077	32.264	15	38455000	20848000	17607000	629	443;1778;1	True;True;	443;1778;1	732;733;28
22.988	201	201;185;18	6.93E-32	0.76485	0.95777	-0.06225	17.152	7	26621000	14628000	11993000	76	255;314;19	True;True;	255;314;19	428;532;30
26.706	252	252;252;22	0.010364	0.73338	0.95743	-0.06276	6.9199	3	2465700	1397000	1068700	228	1966	TRUE	1966	3084;3085
36.053	335	335;335;29	2.34E-115	0.77062	0.95668	-0.06389	11.13	41	263490000	1.46E+08	1.18E+08	600	101;1005;1	True;True;	101;1005;1	168;169;17
117.85	1058	1058;603;5	1.97E-196	0.75467	0.95619	-0.06463	4.7473	37	70970000	39116000	31854000	853	28;73;219;	True;True;	28;73;219;	35;36;37;3
55.011	504	504;313;29	2.31E-06	0.79999	0.95531	-0.06596	2.7372	2	4172700	2269300	1903400	122	1450;1713	True;True	1450;1713	2281;2687
28.768	261	261	4.13E-73	0.76264	0.95355	-0.06862	13.342	13	44788000	24457000	20330000	335	60;380;519	True;True;	60;380;519	101;102;10
32.418	273	273;272;25	8.36E-18	0.77098	0.95327	-0.06904	9.8861	2	7249900	4041700	3208200	454	1297;1550	True;True	1297;1550	2032;2429
20.17	184	184;154;15	1.28E-07	0.71213	0.95223	-0.07062	4.9278	4	12034000	6995600	5038100	750	653;1916;2	True;True;	653;1916;2	1031;1032
13.527	118	118;108;11	3.78E-35	0.71158	0.9515	-0.07172	8.6127	6	8063600	4854700	3208900	281	662;1028;2	True;True;	662;1028;2	1042;1628
25.059	218	218	2.77E-33	0.76457	0.94984	-0.07424	0.28011	2	7023100	3941000	3082100	483	775;3392	True;True	775;3393	1227;5373
30.692	268	268;220	5.93E-11	0.77253	0.94937	-0.07496	9.296	2	3558600	1884400	1674200	526	525;1414	True;True	525;1414	832;2228
76.149	707	707;669	3.39E-32	0.73673	0.94823	-0.07669	9.7362	12	22683000	12783000	9900100	182	250;361;86	True;True;	250;361;86	419;420;60
59.755	527	527	4.18E-16	0.71133	0.94752	-0.07777	12.207	3	5496300	3055300	2441100	813	52;100;500	True;True;	52;100;500	87;167;804
45.374	391	391;383;36	5.16E-41	0.74324	0.94724	-0.0782	8.8044	9	43181000	24422000	18758000	364	990;1089;1	True;True;	990;1089;1	1559;1560
49.203	439	439	8.26E-46	0.73658	0.94662	-0.07914	6.6327	6	16760000	9389600	7370000	290	568;1643;2	True;True;	568;1643;2	897;2588;3
21.119	186	186;176;17	0.0003	0.76895	0.94535	-0.08108	0.84469	2	1820400	998670	821730	227	1294;3189	True;True	1294;3190	2026;5039
20.828	179	179;168;12	3.66E-20	0.74177	0.94516	-0.08137	1.9043	2	10370000	6091000	4279100	593	183;522;16	True;False;	183;522;16	298;299;82
44.819	406	406;314;23	1.98E-61	0.73435	0.94507	-0.08151	3.7923	3	20643000	11542000	9100900	633	776;1846;1	True;True;	776;1846;1	1228;2907
40.816	372	372;370;33	5.90E-21	0.7349	0.94416	-0.0829	31.403	4	9249800	5207900	4041800	356	639;2500;2	True;True;	639;2500;2	1015;3874
33.395	299	299	1.58E-21	0.79007	0.94347	-0.08395	1.8112	3	4719600	2573900	2145600	659	1939;1950	True;True;	1939;1950	3052;3063
223.69	2017	2017	1.84E-07	0.73458	0.94303	-0.08462	6.2329	3	1491200	838530	652620	524	104;2712;3	True;True;	104;2713;3	174;4242;5
19.891	189	189	7.33E-26	0.75702	0.94046	-0.08856	5.6809	6	38074000	21221000	16853000	695	449;605;69	True;True;	449;605;69	741;963;96
70.051	641	641;641;41	5.56E-66	0.78987	0.93948	-0.09007	8.7725	10	26423000	14451000	11972000	725	305;407;12	True;True;	305;407;12	520;686;68
51.028	464	464;463;44	6.77E-128	0.7394	0.93944	-0.09013	32.86	16	85415000	48159000	37256000	566	491;1182;1	True;True;	491;1182;1	795;1843;1
57.936	531	531;605;53	1.66E-252	0.75411	0.93878	-0.09114	56.906	69	314940000	1.75E+08	1.4E+08	822	64;262;381	True;True;	64;262;381	109;110;43
82.999	763	763;260	3.25E-25	0.76187	0.93836	-0.09179	9.5244	7	7493300	4412500	3080800	467	414;578;97	True;True;	414;578;97	695;926;15
26.528	236	236;233;19	2.21E-10	0.76226	0.93713	-0.09368	2.1165	2	2352400	1302300	1050100	262	2258;3426	True;True	2258;3427	3516;5424
31.324	293	293;293;29	7.02E-25	0.76597	0.93574	-0.09582	5.4831	9	19452000	10853000	8598800	226	313;1187;1	True;True;	313;1187;1	531;1849;1
72.572	648	648;634;60	9.47E-05	0.80976	0.93514	-0.09675	8.935	2	2784200	1554000	1230200	491	1541;2683	True;True	1541;2684	2418;4204

110.5	1020	1020;935	4.65E-90	0.74863	0.93461	-0.09756	15.94	22	51849000	29395000	22454000	590	8;24;793;8	True;True;	8;24;793;8	8;29;1252;
29.841	253	253	1.64E-09	0.76021	0.93423	-0.09815	2.2824	2	2981200	1680900	1300300	70	682;1852	True;True	682;1852	1071;2916
36.071	329	329	1.79E-32	0.74283	0.93362	-0.09909	28.763	4	16948000	9322000	7626400	179	434;3065;3	True;True;	434;3066;3	719;720;48
22.782	205	205;171;18	1.43E-41	0.74266	0.93303	-0.1	10.99	6	31435000	17539000	13896000	393	459;1673;2	True;True;	459;1673;2	753;2634;2
21.057	187	187;196;15	1.29E-92	0.72795	0.93233	-0.10109	10.624	11	45768000	25991000	19777000	613	382;1141;2	True;True;	382;1141;2	629;630;17
29.945	264	264;264;26	0.000141	0.75627	0.93072	-0.10358	4.511	3	4314300	2271900	2042400	793	1803;2877	True;True	1803;2878	2848;2849
51.229	472	472;449;44	1.04E-54	0.72288	0.93054	-0.10386	7.4006	6	26264000	14911000	11353000	233	311;2640;3	True;True;	311;2641;3	527;528;52
59.143	528	528	1.42E-09	0.80393	0.92839	-0.1072	4.6571	3	4377800	2448100	1929700	121	274;2203;2	True;True;	274;2203;2	456;3430;4
47.697	427	427;414;25	5.67E-07	0.7245	0.92732	-0.10886	29.645	2	8113600	4201700	3912000	80	0;2180	True;True	0;2180	0;3377
22.876	204	204;107	2.54E-26	0.74385	0.92676	-0.10973	1.7113	6	14003000	7801400	6201500	142	276;2301;2	True;True;	276;2301;2	459;3581;4
24.653	223	223;209;20	1.08E-07	0.74921	0.92635	-0.11037	1.2906	2	1996500	1148100	848330	186	252;2468	True;True	252;2468	424;3832
26.688	243	243;186;13	2.48E-52	0.76069	0.92565	-0.11146	6.7798	15	44477000	25101000	19376000	193	69;431;727	True;True;	69;431;727	115;116;71
52.314	469	469;425;42	2.52E-11	0.71957	0.92458	-0.11313	3.8141	4	18786000	10763000	8022700	734	2850;2889	True;True	2851;2890	4493;4494
28.218	246	246;72;39	4.55E-22	0.74765	0.92442	-0.11338	27.626	2	2688200	1406600	1281600	573	355;566;22	True;False;	355;566;22	599;894;89
32.66	289	289;178;24	2.37E-53	0.77331	0.92386	-0.11425	28.846	10	26566000	14173000	12393000	248	23;433;483	True;True;	23;433;483	27;28;718;
18.898	165	165;174;17	2.50E-20	0.737	0.92353	-0.11477	7.7653	6	18615000	10617000	7998000	143	56;609;129	True;True;	56;609;129	97;968;969
67.819	577	577;576;20	1.21E-14	0.79887	0.92256	-0.11629	13.928	3	5498600	2548700	2949800	612	186;235;25	True;True;I	186;235;25	315;316;39
37.154	328	328;326;27	2.23E-07	0.84543	0.92233	-0.11665	17.185	2	3442200	1758100	1684100	224	2953	TRUE	2954	4647;4648
35.076	317	317;221;15	3.02E-49	0.77681	0.9211	-0.11857	42.487	11	30286000	16710000	13577000	880	432;454;59	True;True;	432;454;59	716;717;74
41.694	368	368;355;32	1.66E-14	0.73217	0.92022	-0.11995	12.039	2	1436300	798870	637450	616	1009;2090	True;True	1009;2090	1600;3263
71.313	637	637;636;63	1.07E-07	0.79581	0.91902	-0.12183	44.617	3	4752400	2239400	2513000	205	122;534;27	True;True;	122;534;27	208;849;43
25.072	228	228;190	2.75E-08	0.7464	0.91762	-0.12403	14.885	3	3416000	1939500	1476500	469	1351;2393	True;True;	1351;2393	2116;3738
92.888	821	821	1.06E-13	0.73223	0.9167	-0.12548	4.4295	3	2831700	1706600	1125100	466	1329;1489	True;True;	1329;1489	2074;2336
24.146	204	204;174;16	3.69E-05	0.7532	0.91653	-0.12575	1.091	2	1914100	1021700	892420	815	2567;3359	True;True	2567;3360	4010;5320
42.592	380	380	2.11E-55	0.71406	0.91491	-0.1283	15.08	5	22164000	12409000	9755200	404	1777;2361	True;True;	1777;2361	2802;2803
44.078	386	386;375;19	1.19E-11	0.71244	0.91457	-0.12883	15.102	3	4337300	2654200	1683100	279	990;1695;2	False;True;	990;1695;2	1559;1560
43.171	409	409;403;36	5.52E-07	0.732	0.91364	-0.1303	6.2851	3	6541200	3855300	2685900	137	792;1312;2	True;True;	792;1312;2	1251;2049
65.596	605	605;412;16	3.22E-11	0.72113	0.91275	-0.13171	2.5989	2	5065200	2870700	2194400	780	2485;2852	True;True	2485;2853	3857;4497
25.895	232	232;219;18	2.70E-15	0.73807	0.91258	-0.13198	3.8414	2	5815900	3514900	2301000	689	790;3274	True;True	790;3275	1244;5176
33.232	295	295	4.71E-16	0.76181	0.90972	-0.13651	9.1538	3	4589600	2482700	2106900	153	2780;2937	True;True;	2781;2938	4352;4610
65.308	589	589;555;53	3.73E-37	0.76522	0.90812	-0.13905	10.818	10	22422000	12445000	9977100	835	771;1371;1	True;True;	771;1371;1	1223;2152
28.279	263	263;230;21	0.000538	0.7308	0.90789	-0.13941	8.9419	2	1267900	729730	538150	126	203;294	True;True	203;294	342;505
40.763	368	368;337	2.75E-09	0.71925	0.90769	-0.13973	1.888	3	7360500	4147200	3213300	893	1041;3091	True;True;	1041;3092	1654;4885
106.49	959	959;923;76	1.31E-06	0.75148	0.90619	-0.14211	20.766	2	1407600	797370	610270	93	1659;1985	True;True	1659;1985	2614;3110
49.184	440	440;294;24	1.40E-10	0.71586	0.90607	-0.14231	2.3608	2	3468000	2011300	1456700	190	329;3238	True;True	329;3239	551;5128
28.85	254	254;254;25	8.90E-57	0.73855	0.90533	-0.14348	5.0437	11	71125000	39506000	31619000	802	220;955;12	True;True;	220;955;12	375;376;14
51.804	459	459	4.27E-61	0.71508	0.90509	-0.14387	11.103	6	12389000	6885200	5503600	599	185;312;36	True;True;	185;312;36	314;530;60
28.415	255	255;175;15	4.24E-22	0.73105	0.9039	-0.14576	9.9517	4	4586800	2573400	2013400	692	1074;1120	True;True;	1074;1120	1699;1762
25.476	221	221;209;20	3.76E-29	0.78094	0.9038	-0.14592	7.0381	3	11658000	6373000	5285200	108	395;2977;3	True;True;	395;2978;3	658;4689;4
33.67	306	306;293;28	1.32E-16	0.72841	0.90247	-0.14805	12.541	4	5895900	3381600	2514300	575	1048;2110	True;True;	1048;2110	1662;3284
27.518	249	249;235;20	1.55E-13	0.71053	0.90198	-0.14883	18.735	5	30180000	17056000	13124000	75	62;2531;25	True;True;	62;2531;25	105;106;39

73.114	711	711;710;36	1.53E-69	0.71671	0.90196	-0.14886	8.9668	15	31273000	18531000	12742000	825	152;364;36	True;True;	152;364;36	249;609;61
27.547	258	258;200	4.29E-14	0.74052	0.90111	-0.15022	10.309	4	6466000	3709200	2756800	453	750;1876;2	True;True;	750;1876;2	1189;2948
35.18	308	308;271;31	3.00E-59	0.75575	0.90079	-0.15074	5.1257	7	15978000	8789200	7188800	32	845;885;10	True;True;	845;885;10	1315;1379
50.8	456	456;419	9.05E-11	0.93981	0.89998	-0.15204	9.793	3	3897000	1983900	1913100	690	2626;2678	True;True;	2626;2679	4103;4199
22.591	194	194;157;15	9.48E-13	0.73403	0.89878	-0.15396	12.761	6	10677000	5973100	4704100	641	1322;1702	True;True;	1322;1702	2064;2676
21.429	192	192;185;14	3.45E-12	0.73084	0.89849	-0.15443	8.4023	5	8608500	4940800	3667700	177	1654;1693	True;True;	1654;1693	2608;2665
38.434	355	355;336;30	8.69E-30	0.78607	0.8981	-0.15505	29.356	8	63354000	35535000	27820000	443	506;889;10	True;True;	506;889;10	810;811;13
24.279	217	217;196	1.15E-09	0.68801	0.89664	-0.1574	6.7183	3	2923600	1707000	1216700	449	171;511;28	True;True;	171;511;28	278;816;44
19.823	174	174;149;11	1.40E-15	0.67879	0.89643	-0.15774	7.3506	5	29597000	17400000	12198000	827	522;805;16	True;True;	522;805;16	829;1266;2
28.787	251	251;195;15	6.34E-19	0.7501	0.89573	-0.15886	8.4514	3	4092600	2393700	1698900	128	1339;1863	True;False;	1339;1863	2094;2095
29.597	263	263;273;26	1.55E-24	0.72318	0.89566	-0.15898	10.995	6	10610000	6170200	4440000	578	1377;1978	True;True;	1377;1978	2161;3101
112.92	995	995;966;84	1.53E-12	0.75836	0.89448	-0.16088	133.98	4	4514800	2618200	1896600	196	81;1692;22	True;True;	81;1692;22	142;2664;3
19.398	169	169;168;12	7.42E-16	0.72619	0.89278	-0.16362	12.02	4	3903600	2246200	1657400	295	594;890;19	True;True;	594;890;19	945;1393;3
75.491	694	694	5.57E-34	0.78486	0.89193	-0.165	13.292	10	20873000	11479000	9393800	569	643;781;22	True;True;	643;781;22	1020;1233
18.042	158	158;112;80	8.85E-33	0.67211	0.89184	-0.16514	4.5928	4	7061100	4272000	2789100	624	1331;2074	True;True;	1331;2074	2084;3242
26.788	240	240;262;25	2.33E-16	0.71241	0.89174	-0.1653	12.808	3	4671900	2646500	2025400	321	386;1061;1	True;True;	386;1061;1	635;1678;2
65.688	599	599;490;49	2.60E-32	0.73055	0.88915	-0.1695	11.652	18	53448000	30542000	22907000	885	446;964;11	True;True;	446;964;11	736;737;15
25.773	236	236;240;23	2.86E-102	0.71928	0.88901	-0.16973	1.6746	2	23103000	13484000	9619000	871	1851;2512	True;False;	1851;2512	2914;2915
25.145	238	238;238;12	2.46E-88	0.71533	0.88879	-0.17009	8.273	6	63326000	36913000	26413000	896	299;723;95	True;True;I	299;723;95	513;1144;1
20.455	182	182	2.10E-16	0.71206	0.8846	-0.1769	3.6593	4	9063700	5174700	3888900	65	1437;1910	True;True;	1437;1910	2267;3010
47.046	434	434;433;42	2.00E-28	0.68628	0.88259	-0.18018	36.287	4	17359000	11906000	5452800	515	580;1303;2	True;True;	580;1303;2	928;2040;4
21.892	198	198;183;13	1.79E-60	0.70105	0.88172	-0.18161	8.0153	13	48642000	28130000	20513000	423	307;308;67	True;True;	307;308;67	522;523;52
16.323	147	147;126	0.001929	0.72364	0.88123	-0.18241	3.0479	2	7383800	4302000	3081800	754	191	TRUE	191	326;327
82.285	734	734;733;69	0.000155	0.70029	0.8807	-0.18328	3.8021	2	1483200	822050	661140	289	1478;1629	True;True	1478;1629	2317;2565
88.885	793	793	3.21E-12	0.71616	0.87994	-0.18452	7.0799	2	2692100	1437700	1254400	271	1996;3178	True;True	1996;3179	3125;5026
40.411	357	357;339;21	1.01E-78	0.70036	0.87968	-0.18495	13.002	11	27083000	15490000	11593000	784	59;378;41(	True;True;	59;378;41(	100;624;69
38.655	352	352;210;16	5.57E-57	0.72454	0.87855	-0.1868	7.2643	13	43565000	24447000	19118000	890	592;765;83	True;True;	592;765;83	942;943;12
28.861	261	261;218;21	2.04E-13	0.69849	0.87755	-0.18845	5.4313	6	9496800	5655800	3841000	316	158;1013;2	True;True;	158;1013;2	257;1604;1
70.901	607	607;564;53	5.24E-36	0.76849	0.8768	-0.18968	6.6647	4	9024400	5099800	3924600	810	1494;1640	True;True;	1494;1640	2341;2584
25.177	224	224	2.06E-23	0.7181	0.87383	-0.19458	43.385	3	5596800	2627100	2969800	369	367;1224;2	True;True;	367;1224;2	612;1904;3
56.65	533	533;499	1.60E-43	0.70305	0.87311	-0.19576	6.8699	8	17388000	10124000	7263900	191	125;516;10	True;True;	125;516;10	211;821;82
50.808	438	438;436;43	5.03E-28	0.69707	0.87261	-0.19659	3.9932	4	8479500	4805600	3673900	481	2193;3149	True;True	2193;3150	3418;4972
18.012	165	165;129;10	1.28E-68	0.67934	0.87237	-0.19699	11.485	20	115460000	66702000	48760000	791	690;878;13	True;True;	690;878;13	1080;1370
37.432	335	335	2.14E-18	0.76728	0.868	-0.20423	11.151	6	9887800	5401500	4486200	149	377;753;10	True;True;	377;753;10	622;623;11
49.679	451	451;432	7.20E-146	0.67093	0.86641	-0.20688	8.2804	14	90673000	52025000	38648000	579	38;78;296;	True;True;	38;78;296;	60;139;509
32.613	294	294;249;12	1.58E-08	0.67283	0.86619	-0.20724	43.985	3	5708700	2806200	2902400	532	914;1150;1	True;True;	914;1150;1	1427;1797
95.785	858	858;835	3.60E-14	0.69163	0.86588	-0.20776	5.8082	4	7290400	4211300	3079000	373	448;834;15	True;True;	448;834;15	740;1302;2
105.84	953	953;922	0.002682	0.71715	0.8648	-0.20956	2.1648	2	2925900	1632000	1293900	706	579;2309	True;True	579;2309	927;3590
37.497	356	356	2.91E-91	0.77986	0.86469	-0.20975	12.751	12	64374000	35744000	28631000	261	157;801;12	True;True;	157;801;12	255;256;12
28.585	249	249;247;20	4.14E-21	0.72797	0.8639	-0.21106	15.05	6	9859400	5679200	4180300	396	524;770;18	True;True;	524;770;18	831;1222;2
15.747	148	148;136;13	4.44E-28	0.64226	0.86289	-0.21275	2.8197	2	6870200	4191200	2679000	758	840;1592	True;True	840;1592	1310;2492

49.973	461	461	2.42E-16	0.66831	0.86235	-0.21365	10.587	3	9208300	5064900	4143300	831	761;768;31	True;True;	761;768;31	1202;1219
33.824	302	302	7.62E-12	0.74494	0.86214	-0.21401	7.3266	5	10715000	6239800	4474700	672	11;3105;34	True;True;	11;3106;34	14;4904;49
23.838	226	226;93;88	0.003281	0.64929	0.86109	-0.21576	63.612	2	841590	475240	366340	178	3272	TRUE	3273	5173;5174
36.824	341	341;328;39	2.25E-29	0.687	0.85993	-0.21771	1.7646	2	3871600	2344700	1526900	488	1031;1422	True;True	1031;1422	1632;2243
95.907	853	853;808	1.51E-11	0.69313	0.85852	-0.22008	3.2056	3	3192000	1874100	1317900	219	1024;1808	True;True;	1024;1808	1618;2856
38.651	366	366;365;36	2.26E-65	0.77649	0.8576	-0.22162	11.703	8	21448000	11951000	9497100	204	156;801;12	True;False;	156;801;12	253;254;12
62.639	543	543;590;51	6.62E-100	0.741	0.85573	-0.22477	13.699	17	70113000	39876000	30237000	234	2;178;231;	True;True;	2;178;231;	2;287;390;
27.764	245	245;149	9.59E-100	0.69048	0.85374	-0.22813	13.637	6	22894000	13171000	9723000	285	356;566;77	True;False;	356;566;77	600;894;89
78.839	689	689;258	1.33E-15	0.66472	0.85239	-0.23041	9.2929	3	2399400	1387200	1012200	829	994;2298;2	True;True;	994;2298;2	1567;3575
38.845	372	372;320;26	4.45E-09	0.67755	0.85157	-0.2318	4.5763	2	3926700	2230500	1696200	564	606;2235	True;True	606;2235	965;3483
34.746	312	312;230	1.21E-05	0.67979	0.85091	-0.23292	10.597	2	843580	464800	378780	677	1765;1914	True;True	1765;1914	2781;3015
29.032	248	248;248;23	1.22E-14	0.6522	0.84963	-0.23509	7.7994	5	10551000	6325300	4225900	589	784;1495;1	True;True;	784;1495;1	1236;2342
35.943	330	330;309;27	1.32E-15	0.71117	0.84924	-0.23576	3.3871	3	3069100	1761700	1307400	251	1122;1154	True;True;	1122;1154	1764;1803
51.782	460	460;210;18	3.83E-08	0.67469	0.84765	-0.23846	3.4755	3	3688000	2108700	1579200	247	893;894;93	True;True;	893;894;93	1396;1397
17.276	148	148;146;10	1.24E-06	0.63361	0.84723	-0.23917	14.927	2	2781200	1706500	1074700	495	1375;1383	True;True	1375;1383	2159;2177
59.004	524	524;510;50	3.04E-16	0.69985	0.84703	-0.23952	10.99	5	7760600	4485500	3275100	836	421;752;11	True;True;	421;752;11	703;704;11
25.834	236	236;235	3.44E-109	0.68891	0.84695	-0.23965	7.7404	12	53990000	31733000	22256000	872	954;2512;2	True;True;	954;2512;2	1493;1494
25.357	239	239;190;11	7.30E-13	0.68409	0.84687	-0.23979	7.3215	3	5099000	3007600	2091400	36	1625;2405	True;True;	1625;2405	2561;3752
48.227	443	443;423;41	0.001446	0.67502	0.84612	-0.24107	2.4383	2	2462600	1467800	994830	150	1431	TRUE	1431	2256;2257
23.819	212	212;188;19	2.03E-06	0.68635	0.8438	-0.24503	15.697	3	1678300	1012800	665510	231	1002;3285	True;True;	1002;3286	1579;5199
34.559	309	309;182	2.40E-21	0.66696	0.8417	-0.24862	4.4803	2	1613000	960610	652380	165	935;2908	True;True	935;2909	1470;4572
44.468	378	378	6.76E-51	0.65386	0.84152	-0.24893	0.79347	3	15252000	9204900	6046600	217	1768;1934	True;True	1768;1934	2784;2785
59.271	546	546;347	1.66E-09	0.69727	0.84076	-0.25023	6.3298	2	2875900	1640900	1235000	110	181;2353	True;True	181;2353	291;3672
38.996	353	353;326	4.74E-14	0.66747	0.83891	-0.25341	6.3709	2	2463100	1564600	898510	715	411;2558;3	True;True;	411;2558;3	692;3982;4
60.134	535	535;528;52	3.42E-06	0.72494	0.83483	-0.26045	8.5961	2	3208400	1968000	1240300	399	2084;2904	True;True	2084;2905	3257;4565
31.279	282	282;225	1.01E-05	0.72097	0.8344	-0.26119	15.691	3	6531800	3778800	2753000	207	837;1157	True;True	837;1157	1306;1307
57.398	517	517;217	3.06E-09	0.64891	0.83302	-0.26358	5.0265	2	2917000	1722700	1194300	448	833;1557	True;True	833;1557	1301;2437
53.376	528	528;525;52	4.33E-14	0.7632	0.83155	-0.26613	15.584	3	9789700	5596800	4193000	649	13;14;181	True;True;	13;14;181	16;17;286
36.573	325	325	1.98E-10	0.65751	0.82977	-0.26922	11.333	3	3158700	1867800	1290900	628	1105;2590	True;True;	1105;2590	1743;4044
24.579	218	218;218	1.07E-07	0.67388	0.82847	-0.27148	4.7838	3	1911900	1053800	858150	591	882;2262;3	True;True;	882;2262;3	1376;3522
19.329	164	164;124	9.73E-10	0.60291	0.82831	-0.27176	20.037	3	5876900	3445300	2431600	173	83;2228;22	True;True;	83;2228;22	144;3475;3
16.801	142	142;154;15	2.89E-18	0.62341	0.82329	-0.28053	9.5615	3	4936000	3075200	1860800	441	984;2065;2	True;True;	984;2065;2	1548;3233
51.556	437	437;428;34	0.001835	0.68013	0.8201	-0.28613	14.308	2	2196500	1331300	865150	614	542;3136	True;True	542;3137	860;4951
50.679	443	443;428;32	7.59E-11	0.64005	0.81971	-0.28681	10.849	3	12089000	7236100	4853300	845	729;1101;2	True;True;	729;1101;2	1155;1739
15.936	154	154;135	3.77E-12	0.61798	0.81613	-0.29313	1.5672	3	8060800	4987400	3073400	595	1022;1276	True;True;	1022;1276	1616;1997
51.026	461	461;355	6.44E-07	0.64543	0.81608	-0.29322	1.2066	2	6158400	3718500	2439900	168	404	TRUE	404	677;678
29.909	260	260;252	4.93E-16	0.69373	0.81555	-0.29415	3.968	4	3678800	2111500	1567300	522	1168;1509	True;True;	1168;1509	1817;2371
82.588	737	737;317	4.19E-17	0.65066	0.81499	-0.29515	4.7225	3	3454800	2150300	1304400	319	1032;1664	True;True;	1032;1664	1633;2619
47.535	440	440;429	0.000159	0.63837	0.81444	-0.29612	37.162	3	6070200	3326500	2743700	215	1374;2325	True;True	1374;2325	2157;2158
42.942	378	378;377	4.74E-15	0.85357	0.81162	-0.30112	4.4737	4	10375000	5422000	4952800	748	1542;1896	True;True;	1542;1896	2419;2995
77.515	730	730;691	7.72E-08	0.65828	0.81077	-0.30264	26.311	2	3282500	2000500	1282000	537	84;1463	True;True	84;1463	145;2298

40.542	367	367;235	6.62E-08	0.85244	0.81054	-0.30304	0.29834	2	2606500	1369700	1236800	475	1353;1493	True;True	1353;1493	2121;2340	
45.566	398	398;364	1.09E-19	0.84831	0.80949	-0.30491	1.1156	2	2305600	1201300	1104400	283	747;2141	True;True	747;2141	1185;3330	
88.549	835	835;753	2.08E-13	0.65649	0.80662	-0.31004	10.695	2	3695500	2269500	1426000	796	1690;1981	True;True	1690;1981	2662;3106	
36.726	325	325;289	1.95E-26	0.69559	0.80502	-0.3129	2.3354	3	5602400	3258700	2343700	729	1317;1341	True;True;	1317;1341	2058;2098	
45.199	427	427;162	9.47E-82	0.84003	0.80443	-0.31396	12.358	9	21695000	11926000	9769600	460	451;650;89	True;True;	451;650;89	743;1028;1	
45.594	417	417;345;35	1.82E-12	0.68288	0.80362	-0.31541	23.291	3	8041100	4037200	4003900	552	1977;2099	True;True	1977;2099	3099;3100	
25.734	231	231	1.57E-07	0.65999	0.80312	-0.31631	6.3788	2	6443000	4058700	2384300	245	161;3258	True;True	161;3259	263;5155	
90.583	825	825;806;78	3.86E-23	0.62967	0.79478	-0.33137	9.3265	8	10386000	6268500	4117400	823	466;725;90	True;True;	466;725;90	761;1150;1	
42.153	407	407;386	6.09E-06	0.71406	0.79433	-0.33219	28.492	2	2842800	1636800	1206000	482	2610	TRUE	2610	4071;4072	
33.186	300	300;283;15	1.65E-09	0.66749	0.79213	-0.33619	8.4198	2	2229700	1320400	909240	198	1361	TRUE	1361	2139;2140	
63.826	561	561;545;51	6.40E-08	0.60853	0.78117	-0.35629	4.447	2	2091900	1281300	810600	565	450;1230	True;True	450;1230	742;1911	
46.247	413	413;366	9.12E-67	0.81682	0.77943	-0.35951	6.61	10	18871000	10635000	8236300	601	268;1345;1	True;True;	268;1345;1	449;450;21	
33.488	290	290;277;26	2.54E-31	0.78968	0.77778	-0.36257	11.713	6	45285000	24690000	20595000	501	667;1310;1	True;True;	667;1310;1	1048;1049	
49.924	448	448;433;26	3.03E-127	0.60492	0.77654	-0.36487	13.873	5	16139000	9775500	6363700	131	333;339;65	False;True;	333;339;65	557;565;56	
59.717	542	542;537;53	8.38E-12	0.67197	0.77601	-0.36585	10.524	3	2823500	1621800	1201800	291	482;629;24	True;True;	482;629;24	783;1005;3	
36.926	346	346;331;29	2.51E-11	0.61741	0.77598	-0.36591	6.6212	2	1464900	948140	516790	232	310;2639	True;True	310;2640	526;4122	
42.613	376	376;335;37	4.47E-34	0.80141	0.77412	-0.36937	12.162	5	12989000	7060200	5928500	447	107;287;55	True;True;	107;287;55	186;187;49	
30.375	277	277;222;17	2.27E-21	0.62397	0.7715	-0.37426	13.94	2	2532300	1504700	1027600	684	847;1156	True;True	847;1156	1317;1805	
37.429	353	353;317;34	1.67E-20	0.63437	0.77058	-0.37598	14.314	6	14793000	9016800	5776100	765	1072;1318	True;True;	1072;1318	1696;1697	
48.408	451	451;336;28	1.52E-71	0.78857	0.75515	-0.40516	2.4087	2	18980000	10564000	8416000	785	1220;2849	True;True;	1220;2850	1897;4492	
39.589	359	359;314;28	3.64E-11	0.61312	0.75266	-0.40993	0.97852	2	1783300	1069100	714180	730	222;988	True;True	222;988	380;1554	
40.589	351	351;343;39	1.61E-10	0.78712	0.74844	-0.41804	4.3955	2	3054800	1722900	1331900	585	1442;2199	True;True	1442;2199	2273;3424	
45.796	403	403;389;38	6.43E-37	0.77646	0.7383	-0.43772	11.084	3	7684300	4396600	3287600	340	228;832;12	True;True;	228;832;12	387;1300;1	
38.274	338	338	1.62E-22	0.76852	0.73595	-0.44232	8.569	3	9991500	5475800	4515700	462	810;1088;1	True;True;	810;1088;1	1271;1723	
26.183	228	228;223;18	1.72E-22	0.57518	0.72812	-0.45775	8.2716	6	12312000	7869900	4441900	296	646;647;71	True;True;	646;647;71	1023;1024	
45.26	418	418;364;36	6.17E-132	0.73986	0.72788	-0.45823	20.333	25	255160000	1.42E+08	1.13E+08	814	25;39;173;	True;True;	25;39;173;	30;31;32;6	
35.611	320	320;144	2.50E-12	0.75623	0.71906	-0.47582	6.6834	3	5086500	2945500	2141000	660	728;1919;3	True;True;	728;1919;3	1154;3021	
64.615	592	592;591;23	3.55E-74	0.60682	0.70897	-0.4962	8.1966	16	53564000	32848000	20716000	657	193;253;26	True;True;	193;253;26	329;425;43	
27.366	238	238;235;16	1.36E-08	0.60047	0.70591	-0.50244	4.3418	2	2722800	1644200	1078600	68	97;2228;32	True;False;	97;2228;32	160;3475;5	
38.242	331	331;282;21	6.73E-30	0.7369	0.70566	-0.50295	17.577	5	12031000	6774200	5256700	834	764;1160;1	True;True;	764;1160;1	1205;1809	
27.557	264	264	1.50E-82	0.58685	0.70314	-0.50812	3.303	7	32831000	19824000	13008000	735	2379;2560	True;True	2379;2560	3701;3702	
43.062	390	390;150;11	3.73E-67	0.72199	0.70112	-0.51227	30.391	9	34929000	19975000	14953000	99	1433;2233	True;True;	1433;2233	2259;2260	
76.613	710	710;603;48	2.07E-130	0.57235	0.70048	-0.51358	100.8	34	151380000	94501000	56878000	842	187;240;24	True;True;	187;240;24	317;318;31	
69.842	609	609;557;56	8.33E-22	0.5562	0.69669	-0.52141	10.667	5	11837000	7483900	4353400	851	561;1425;2	True;True;	561;1425;2	888;889;22	
21.007	188	188;127;94	6.24E-10	0.56341	0.69265	-0.5298	55.021	3	4504900	2623200	1881700	468	142;2581;3	True;True;	142;2581;3	234;4032;5	
31.999	292	292;248;20	9.09E-17	0.59041	0.69119	-0.53285	4.9761	5	9215600	5941900	3273700	558	457;463;46	True;True;	457;463;46	750;751;75	
35.967	332	332;329;28	2.69E-21	0.71746	0.6822	-0.55173	29.3	3	10913000	5921800	4991300	744	1051;1343	True;True	1051;1343	1665;2100	
65.401	586	586;579;56	2.83E-37	0.69436	0.6756	-0.56576	13.383	8	22555000	12942000	9612800	803	50;272;90	True;True;	50;272;90	85;454;142	
51.092	449	449;389	3.01E-10	0.69607	0.66421	-0.59029	0.50255	2	2895500	1676800	1218700	189	5;1332	True;True	5;1332	5;2085	
22.58	226	226	8.11E-13	0.53576	0.65502	-0.61039	15.369	6	27765000	18017000	9748200	583	168;317;15	True;True;	168;317;15	274;275;53	
22.35	221	221;219;21	1.28E-18	0.53386	0.64913	-0.62342	12.51	11	31325000	20266000	11059000	582	165;295;15	True;True;	165;295;15	269;270;27	